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Sequence 85, Application US/10735916A Publication No. US20050084906A1
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109, App
26, Appl
25, Appl
29, Appl
127, App
111, Appl
24, Appl
24, Appl
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5, Appli
                                                    January 10, 2006, 20:53:43; Search time 64.1754 Seconds (without alignments) 761.757 Million cell updates/sec
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(cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
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; (cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
; (cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
; (cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
; (cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
; (cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd
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US-10-735-916A-85
US-10-735-916A-87
US-10-735-916A-75
US-10-735-916A-75
US-10-735-916A-75
US-10-735-916A-69
US-10-735-916A-69
US-10-392-088-109
US-10-805-177-56
US-10-805-177-56
US-10-805-177-56
US-10-309-762-25
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Listing first 45 summaries
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138, App
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98, Appl
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14, Appl
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Sequence 83, Application US/10735916A

Publication No. US20050084906A1

GENERAL INFORMATION:
APPLICANT: GOSTSCH, Liliane
APPLICANT: CORVALA, Nathalie
APPLICANT: LEGER, Olivier
APPLICANT: DUFLOS, Alain
APPLICANT: DUFLOS, Alain
APPLICANT: HAEUW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-183
CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT APPLICATION NUMBER: US/10/735,916A
FRIOR PRICA APPLICATION NUMBER: PC7/FR 03/00 538
PRIOR FILING DATE: 2003-07-11
PRIOR PLING DATE: 2003-01-20
PRIOR PLING DATE: 2003-01-20
PRIOR PLING DATE: 2002-01-18
PRIOR PLING DATE: 2002-01-18
PRIOR FILING DATE: 2002-05-07
NUMBER OF SEQ ID NOS: 156
SOPTWARE: PATENTIN VET: 2.1
FURNATION NUMBER: FR 02/05 753
FROM APPLICATION NUMBER: FR 02/05 533
FRIOR PRILOR PATE: 2002-05-07
NUMBER OF SEQ ID NOS: 156
SSO ID NOS: 156
SSO ID NO 93
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US-10-984-960A-20
US-10-893-576-39
US-10-805-177-12
US-10-805-177-12
US-10-805-177-12
US-10-292-088-98
US-10-292-088-70
US-10-822-306A-14
US-10-822-306A-14
US-10-822-306A-19
US-10-822-306A-11
US-10-822-306A-11
US-10-822-306A-11
US-10-292-088-142
US-10-292-088-66
US-10-292-088-66
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US-10-684-109-3
US-10-684-109-3
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    type: PRT
CRGANISM: Homo sapiens
US-10-735-916A-83
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Publication No. US20050084906A1

GENERAL INFORMATION:

APPLICANT: GOBTSCH. Liliane

APPLICANT: CORVAIA, Nathalie

APPLICANT: CORVAIA, Nathalie

APPLICANT: BECER, Olivier

APPLICANT: BECK, Alain

TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF

FILE REFERENCE: 017753-183

TITLE OF INVENTION: NUMBER: US/10/735, 916A

CURRENT APPLICATION NUMBER: FR 03/08 538

FRIOR APPLICATION NUMBER: FR 02/08 653

FRIOR FILING DATE: 2003-07-11

FRIOR PELING DATE: 2003-01-20

FRIOR PELING DATE: 2003-01-18

FRIOR FILING DATE: 2002-01-18

FRIOR 
       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GORTSCH, Liliane
APPLICANT: CORVALA, Nathalie
APPLICANT: LEGER, Olivier
APPLICANT: DUFLOS, Alain
APPLICANT: DUFLOS, Alain
APPLICANT: HAEUW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-183
CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT FILING DATE: 2003-07-11
FRIOR APPLICATION NUMBER: PR 03/08 538
FRIOR FILING DATE: 2003-07-11
FRIOR APPLICATION NUMBER: PR 02/00 653
FRIOR APPLICATION NUMBER: PR 02/00 653
FRIOR APPLICATION NUMBER: FR 02/00 654
FRIOR APPLICATION NUMBER: FR 02/00 654
FRIOR PILING DATE: 2002-01-18
FRIOR PILING DATE: 2002-01-18
FRIOR FILING DATE: 2002-05-07
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PACENT IN VET. 2.1
SEQ ID NO 85
LENGTH: 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-85
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ORGANISM: Homo sapiens
GENERAL INFORMATION:
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US-10-735-916A-79
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                                                                                                                                                                                                                                                                                  61 KPSLKDRVTISVDTSKNQPSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
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APPLICANT: GOSTSCH, Liliane
APPLICANT: GOSTSCH, Liliane
APPLICANT: GOSTSCH, Liliane
APPLICANT: GOSTSCH, Liliane
APPLICANT: BESER, Alain
APPLICANT: UNWELL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE OF INVENTION NUMBER: EN 03/00 538
FRIOR PELING DATE: 2003-01-1
FRIOR APPLICATION NUMBER: PCT/FR 03/00 178
FRIOR PILING DATE: 2002-01-18
FRIOR APPLICATION NUMBER: FR 02/00 653
FRIOR PELING DATE: 2002-01-18
FRIOR PILING DATE: 2002-01-18
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Sequence 75, Application US/10735916A

Sequence 75, Application US/10735916A

Publication No. US20050084906A1

GENERAL INFORMATION:
APPLICANT: CORVIA, Nathalie
APPLICANT: LEGER, Olivier
APPLICANT: BECK, Alain
APPLICANT: BECK, Alain
APPLICANT: HEUW, Jean-Francois
APPLICANT: HEUW, Jean-Francois
APPLICANT: HEUW, Jean-Francois
APPLICANT: HEUW, Jean-Francois
APPLICANT: HILL OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
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Pred. No. 4.5e-47;
1; Mismatches 1; Indels
       Length 117;
                                                                         1; Indels
   Score 615; DB 5;
Pred. No. 3.9e-47;
1; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 81, Application US/10735916A Publication No. US20050084906A1
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98.3%;
   98.4%;
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Best Local Similarity 98.3%
Matches 115; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 81
Query Match
Best Local Similarity 98.3
Matches 115; Conservative
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; ORGANISM: Homo sapiens
US-10-735-916A-81
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19 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 77, Application US/10735916A
Publication No. US20050084906A1
GENERAL INFORMATION:
APPLICANT: CORTSCH.
APPLICANT: CORVAIA, Nathalie
APPLICANT: LEGER, Olivier
APPLICANT: DUFLOS, Alain
APPLICANT: HAEUW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-183
CURRENT APPLICATION NUMBER: US/10/735,916A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 97.8%; Score 611; DB 5; Length 117; Best Local Similarity 96.6%; Pred. No. 8.8e-47; Matches 113; Conservative 3; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2003-12-16
PRIOR APPLICATION NUMBER: FR 03/08 538
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-01-20
PRIOR FILING DATE: 2003-01-20
PRIOR FILING DATE: 2002-01-18
                  CURRENT PEDELICATION NUMBER: US/10/735,916A
CURRENT FILING DATE: 2003-12-16
PRIOR PRIOR PILING DATE: 2003-12-16
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-01-20
PRIOR PILING DATE: 2003-01-20
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 02/00 654
PRIOR APPLICATION NUMBER: FR 02/00 654
PRIOR APPLICATION NUMBER: FR 02/05 753
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-05-07
NUMBER OF SEQ ID NOS: 156
SEQ ID NO 75
LENGTHALLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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US-10-735-916A-77
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2 VQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNYK 61
61 KPSLKDRVTISVDTSKNOFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                          79 KPSLKDRITISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VOLGESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIROPPGKGLEWIGYISYDGTNNYK
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APPLICANT: CORVAIA, Nathalie

APPLICANT: CORVAIA, Nathalie

APPLICANT: CORVAIA, Nathalie

APPLICANT: BEGER, Olivier

APPLICANT: BEGER, Alain

APPLICANT: BECK, Alain

APPLICANT: MAEUW, Jean-Francois

TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF

FILE REPERRNCE: 01753-131

CURRENT FILING DATE: 2003-12-16

PRIOR APPLICATION NUMBER: PR 03/08 538

PRIOR PILING DATE: 2003-07-11

PRIOR FILING DATE: 2003-01-20

PRIOR FILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-05-07
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Fublication No. US20050084906A1
GENERAL INFORMATION:
APPLICANT: GORTSCH, Liliane
APPLICANT: CORVAIA, Nathalie
APPLICANT: LEGER, Olivier
APPLICANT: DUFLOS, Alain
APPLICANT: BECK, Alain
FILE OF INVENTION NUMBER: US/10/35,916A
CURRENT APPLICATION NUMBER: PR 03/08 538
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-07-12
PRIOR FILING DATE: 2003-01-20
PRIOR FILING DATE: 2003-01-20
PRIOR FILING DATE: 12003-01-20
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                                                                                                                                                                                                                                             Sequence 69, Application US/10735916A Publication No. US20050084906A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 156
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Mus musculus US-10-735-916A-69
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                                                                                                                                                                                                                                                                                                                                                                                                                 12 VQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNYK 71
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; Sequence 143, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Golds, Jean
APPLICANT: Hands, Masshisa
APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTHRODIES AGAINST CARBOXIC ANHYDRASE IX
ITLE OF INVENTION: ANTHRODIES AGAINST CARBOXIC ANHYDRASE IX
FILE REFERENCE: ABGENIX.027A
CURRENT FALING DATE: 2002-12-02
FILE REPERIOR NUMBER: 60/337275
PRIOR APPLICATION NUMBER: 60/337275
; PRIOR APPLICATION NUMBER: 60/337275
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 143
; LENGTH: 119
                                                                                                                                                                                                                                                                                       Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.7%; Score 517; DB 4; Length 119;
85.0%; Pred. No. 2.1e-38;
tive 4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                               9; Indels
                                                                                                                                                                                                                                                                                    Query Match

84.6%; Score 529; DB 5;
Best Local Similarity 82.8%; Pred. No. 1.9e-39;
Matches 96; Conservative 11; Mismatches 9.
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 52
; SEQ ID NO 52
; LENGTH: 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 85.09
Matches 102, Conservative
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CORGANISM: Mus musculus
US-10-735-916A-52
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ORGANISM: Homo sapiens
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US-10-292-088-109
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US-10-383-447-26

i Sequence 26, Application US/10383447

i Publication No. US20040096392A1

i GENERAL INFORMATION:

APPLICANT: Bhaskar, Vinay

APPLICANT: de la Calle, Agustin

APPLICANT: Caras, Ingrid

APPLICANT: Ramakrishnan, Vanitha

APPLICANT: Ramakrishnan, Vanitha

APPLICANT: Afar, Daniel

APPLICANT: Powers, David

APPLICANT: Murray, Richard

APPLICANT: With antibodies Against Cancer Antigen TWEFF2 and Uses Thereof

CURRENT APPLICATION NUMBER: US/10/383,447

CURRENT PILING DATE: 2002-03-07

PRIOR PILING DATE: 2002-03-08

PRIOR PILING DATE: 2002-12-27

NUMBER OF SEQ ID NOS: 34

SOFTHARE: Patentin version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGYIYYSGSTNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                    82.3%; Score 514.5; DB 4; Length 118; 85.7%; Pred. No. 3.5e-38; Live 3; Mismatches 11; Indels 3.
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                    FILE REFERENCE: ABX-PF/3 US
CURRENT APPLICATION NUMBER: US/10/292,088
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 60/348,980
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 147
SOFTWARE: Patentin Ver. 2.1
TITLE OF INVENTION: ANTIBODIES TO CD40
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 85.73
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-10-292-088-109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 98; Conserv
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                                                                                                                                                                                                                                                       LENGTH: 118
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LENGTH: 120
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US-10-805-177-56

RESULT 12

Sequence 109, Application US/10292088
Publication No. US20030211100A1
GENERAL INFORMATION:
APPLICANT: BEDIAN, VAHE
APPLICANT: GLADUE, RONALD P.
APPLICANT: CONVALAN, JOSE
APPLICANT: FENG, XIAO-CHI
APPLICANT: FENG, XIAO-CHI

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60 NPSLKSRVTISVDISKNQPSLKLSSVTAADTAVYYCARRGYDFLIGYDYFDYWGQGILVI 119
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Sequence 128, Application US/10309762

Publication No. US20040018198A1

GENERAL INFORMATION:

APPLICANT: Gudae, Jean

APPLICANT: Handa, Jean

APPLICANT: Gallo, Michael

TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX

TITLE OF INVENTION: ANTIBODIES

CURRENT APPLICATION NUMBER: US/10/309,762

CURRENT FILING DATE: 2002-12-02

PRIOR APPLICATION NUMBER: 60/337275

FRIOR APPLICATION NUMBER: 60/337275

SPIOR APPLICATION NUMBER: 2010-12-03

NUMBER OF SEQ ID NOS: 246

SOPTWARE: FRAESE for Windows Version 4.0

SEQ ID NO 128
                                                                                                                                                                                                                                                                                                            US-10-309-762-29

is Sequence 29, Application US/10309762

is Publication No. US20040018198A1

is GENERAL INFORMATION:

is APPLICANT: Gudae, Jean

APPLICANT: Handa, Masahisa

APPLICANT: Handa, Masahisa

is APPLICANT: Gallo, Michael

is TILLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX

TILLE OF INVENTION: ANTIBODIES

TILLE OF INVENTION: ANTIBODIES

TILLE OF INVENTION: ANTIBODIES

TILLE OF INVENTION: AND ADDIES

FILE REFERENCE: ABGENIX.027A

CURRENT FILING DATE: 2002-12-02

PRIOR APPLICATION NUMBER: 60/337275

PRIOR FILING DATE: 2001-12-03

NUMBER OF SEQ ID NOS: 246

SOFTWARE: FastERQ for Windows Version 4.0

SEQ ID NO 29
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61 KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRVF
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US-10-309-762-128
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US-10-309-762-128
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                                         PUDLICATION NO. US20050084449A1

GENERAL INFORMATION:

APPLICANT: Landes, Gregory M.

APPLICANT: Landes, Binyam

APPLICANT: Ghen, Francine

APPLICANT: Foltz, Ian

APPLICANT: Tee, Kam Fai

APPLICANT: Tee, Kam Fai

APPLICANT: Aleffers, Michael

APPLICANT: Gregory, Michael

APPLICANT: Gregory, Michael

APPLICANT: Meses, Peter

APPLICANT: Khramtsov, Nikolia

TITLE OF INVENTION: DOMAIN AND MUCIN DOMAIN 1 (TIM-1) ANTIGEN AND USES THEREOF

FILE REFERENCE: ALONGE: 2004-03-19

CURRENT APPLICATION NUMBER: US/10/805,177

CURRENT FILING DATE: 2004-03-19

NUMBER OF SEQ ID NOS: 141

NUMBER OF SEQ ID NOS: 141

NUMBER OF SEQ ID NOS: 141

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; Publication No. US20040018198A1
; GRERAL INFORMATION:
APPLICANT: Galds, Jean
APPLICANT: Foltz, Ian
; APPLICANT: Holds, Masahisa
APPLICANT: Holds, Masahisa
TITLE OF INVENTION: (CA.IX) TUMOR ANTIGEN
; TITLE OF INVENTION: (CA.IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; RIGH RILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 25
; LENGTH 122
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   Sequence 56, Application US/10805177
Publication No. US20050084449A1
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Matches 103; Conservative
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; ORGANISM: Homo sapiens
US-10-309-762-25
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ORGANISM: Homo Sapiens
US-10-805-177-56
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LENGTH: 121
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        Query Match
        82.0%;
        Score 512.5;
        DB 4;
        Length 120;

        Best Local Similarity
        85.0%;
        Pred. No. 5.3e-38;
        Anismatches 102;
        Conservative 4;
        Mismatches 11;
        Indels 3;
        Gaps 2;

        Qy
        1 QVQLQBSGPGLVKPSETLSLTCTVSGVS-ISGGYLWWIRQPEGGLEWIGYISYDGTNN 59
        Indels 3;
        Gaps 2;

        Db
        1 QVQLQBSGPGLVKPSETLSLTCTVSGVS-ISGGYLWWIRQPEGGLEWIGYISYSGSN 60
        Go
        CO

        CQ
        CO
        VKPSIKSRVTISVDTSKNQFSIKLSSVTAADTANYYCAR--YGRVFFDYWGGGTLVTVSS 117
        Indels 111

        Db
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        Indels 111
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Search completed: January 10, 2006, 21:35:33 Job time : 64.1754 secs

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69, Appl
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73, Appl
1651, Ap
1548, Ap
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17, Appl
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1329, Ap
112, App
110, App
70, Appl
990, App
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1 QVQLQESGPGLVKPSETLSL......RYGRVFFDYWGQGTLVTVSS 117
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GenCore version 5.1.6
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Maximum Match 100%
Listing first 45 summaries
                                                                   protein search, using sw model
                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length DB
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Maximum DB
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## ALIGNMENTS

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SOFTWARE: Pate
SEQ ID NO 81
LENGTH: 135
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## Sequence 85, Application US/11012353

| Sequence 85, Application US/11012353
| Publication No. US20050249730A1
| GENERAL INFORMATION:
| APPLICANT: CORVALA, NATHALIE
| APPLICANT: CORVALA, NATHALIE
| APPLICANT: DUFLOS, ALAIN
| APPLICANT: LEGER, OLIVIER
| APPLICANT: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
| TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
| TILE REFERENCE: 017753-198
| CURRENT APPLICATION NUMBER: US/11/012,353
| CURRENT PILING DATE: 2003-12-16
| PRIOR PILING DATE: 2003-07-11
| PRIOR PILING DATE: 2002-01-20
| PRIOR PILING DATE: 2002-01-20
| PRIOR PILING DATE: 2002-01-18
| NUMBER OF SEQ ID NOS: 162
| SOPTWARE: PRIOR PILING DATE: 2002-01-18
| SEGION NOSE RELIANTOR NOSE RELIANTOR PERSONARE: PRIOR PE
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Publication No. US20050249730A1

GENERAL INFORMATION:

APPLICANT: CORVAIA, NATHALIE

APPLICANT: CORVAIA, NATHALIE

APPLICANT: CORVAIA, NATHALIE

APPLICANT: LEGER, OLIVIER

APPLICANT: ALAIN

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

FILE REFERENCE: 017753-198

CURRENT APPLICATION NUMBER: U0/735,916

PRIOR APPLICATION NUMBER: FR 0308538

PRIOR PLING DATE: 2003-01-20

PRIOR APPLICATION NUMBER: PCT/FR03/00178

PRIOR APPLICATION NUMBER: FR 0205-67-11

PRIOR APPLICATION NUMBER: FC 0205-53
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j Sequence 81, Application US/11012353

publication No. US20050249730A1

j GENERAL INFORMATION:

APPLICANT: GORYALA, NATHALIE

APPLICANT: OGNYALA, NATHALIE

APPLICANT: DIFLOS, ALAIN

APPLICANT: BECK, ALAIN

TITLE OF INVENTION: NOVEE ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: NOVEE ANTIBODIES AND USES THEREOF

TITLE OF INVENTION: NUMBER: US/11/012,353

CURRENT APPLICATION NUMBER: 10/753-196

PRIOR FILING DATE: 2003-12-16

PRIOR FILING DATE: 2003-07-11

PRIOR FILING DATE: 2002-01-18

PRIOR APPLICATION NUMBER: FR 0200553

PRIOR PLING DATE: 2002-01-18

PRIOR APPLICATION NUMBER: FR 0200553

PRIOR PLING DATE: 2002-01-18

PRIOR PLING DATE: 2002-01-18
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PRIOR FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: FR 0200653
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 0200654
PRIOR FILING DATE: 2002-01-18
NUMBER: OF SEQ ID NOS: 162
SOFTWARE: PATENTIN Ver. 3.3
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US-11-012-353-79
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PRIOR APPLICATION NUMBER: FR 0205753
PRIOR FILING DATE: 2002-05-07
PRIOR PELING NUMBER: FR 0200653
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARE: PATENTIN Ver. 3.3
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Best.Local Similarity 88.04
Matches 103; Conservative
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SOFTWARE: Patentin Ver. 3.3
                                                                                                                                                                                                                                                                              , ORGANISM: Homo sapiens
US-11-012-353-77
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US-11-012-353-162
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                                                                                                                                                                                                                                    LENGTH: 135
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                                                                                                                                                                                                                                                              TYPE: PRT
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                                                                                                  Sequence 75, Application US/11012353

Sequence 75, Application US/11012353

Publication No. US20050249730A1

GENERAL INFORMATION:

APPLICANT: GORYSCH, LILIANE

APPLICANT: DUFLOS, ALAIN

APPLICANT: DUFLOS, ALAIN

APPLICANT: BECK, ALAIN

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND USES THEREOF

FILER REFERENCE: 017753-196

FILER REFERENCE: 017753-196

PRIOR APPLICATION NUMBER: US/11/012,353

CURRENT FILING DATE: 2003-12-16

PRIOR FILING DATE: 2003-12-16

PRIOR FILING DATE: 2003-07-11

PRIOR FILING DATE: 2003-07-12

PRIOR FILING DATE: 2003-07-13

PRIOR FILING DATE: 2002-01-18

NUMBER OF SEQ ID NOS: 162

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CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT FILING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: 10/735,916
PRIOR FILING DATE: 2003-12-16
PRIOR APPLICATION NUMBER: FR 0308538
PRIOR FILING DATE: 2003-01-11
PRIOR APPLICATION NUMBER: PR 02047-11
PRIOR APPLICATION NUMBER: PR 02047-11
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Pred. No. 3.7e-47;
3; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: GOETSCH, LILIANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: LEGER, OLIVIER
APPLICANT: BECK, ALAIN
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; ORGANISM: Homo sapiens
US-11-012-353-75
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Best Local Similarity
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APPLICANT: BECK, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-198
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT FILING DATE: 2004-12-16
PRIOR PELING DATE: 2003-12-16
PRIOR APPLICATION NUMBER: PR 0308538
PRIOR APPLICATION NUMBER: PR 0308538
PRIOR PILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: PR 0205753
PRIOR PILING DATE: 2003-06-07
PRIOR PILING DATE: 2003-06-07
PRIOR PILING DATE: 2003-01-18
PRIOR APPLICATION NUMBER: PR 0206553
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
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                                                                                                                                                                                                                                                             61 KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                 79 KPSLKDRITISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 135
                                                                                                                                                                   19 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
                                                                                                                                 1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                     Gaps
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Query Match 97.8%; Score 611; DB 7; Length 135; Best Local Similarity 96.6%; Pred. No. 4.2e-47; Matches 113; Conservative 3; Mismatches 1; Indels
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Pred. No. 1.7e-41;
4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 162, Application US/11012353
Publication No. US20050249730A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: GOETSCH, LILIANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: LEGER, OLIVIER
APPLICANT: BECK, ALAIN
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us-10-735-916a-83.rapbn

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Query Match
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| GENERAL INFORMATION |
| GENERAL INFORMATION |
| APPLICANT: GOEYSCH, LILIANE |
| APPLICANT: GOEYSCH, LILIANE |
| APPLICANT: DUFLOS, ALAIN |
| APPLICANT: LEGER, OLIVIER |
| TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF |
| FILE REFERENCE: 011753-196 |
| FRIOR FILING DATE: 2004-12-16 |
| PRIOR PELICATION NUMBER: FR 0308538 |
| PRIOR PELLING DATE: 2003-01-20 |
| PRIOR APPLICATION NUMBER: FR 0206553 |
| PRIOR APPLICATION NUMBER: FR 0206554 |
| PRIOR APPLICATION NUMBER: FR 0206554 |
| PRIOR FILING DATE: 2002-01-18 |
| PRIOR FILING DATE: 2002-01-18 |
| PRIOR FILING DATE: 2002-01-18 |
| RIOR FILING DATE: 2002-01-18 |
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i Sequence 52, Application US/11012353

j Publication No. US20050249730A1

i GENERAL INFORMATION:
   APPLICANT: GORTSCH, LILIANE
   APPLICANT: CORVAIA. NATHALIE
   APPLICANT: DUFLCS, ALAIN
   APPLICANT: HAEUW, JEAN-FRANCOIS
   TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
   TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
   TITLE OF INVENTION: NOWEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
   TITLE OF INVENTION: NOWEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
   TITLE OF INVENTION: NOWER: 10/735-916
   PRIOR PELING DATE: 2003-12-16
   PRIOR FILLING DATE: 2003-12-16
   PRIOR FILLING DATE: 2003-07-11
   PRIOR FILLING DATE: 2003-07-11
   PRIOR FILLING DATE: 2003-07-11
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61 NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTTLTVSS 117
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Publication No. US20050249730A1
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; ORGANISM: Mus musculus
US-11-012-353-69
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APPLICANT: CORTEN. LILLAND.
APPLICANT: CORTEN. NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
APPLICANT: DUFLOS, ALAIN
APPLICANT: DUFLOS, ALAIN
APPLICANT: DEGER, OLIVIER
APPLICANT: BECK, ALAIN
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
FILE REFERENCE: 01753-198
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT APPLICATION NUMBER: FR 0308538
PRIOR FILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: FR 020653
PRIOR APPLICATION NUMBER: FR 020655
PRIOR APPLICATION NUMBER: FR 020655
PRIOR APPLICATION NUMBER: FR 020655
PRIOR PILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARE: PRICETIN VET. 3.3
SEQ ID NO 73
TENDATAL 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                    84.6%; Score 529; DB 7; Length 127; 82.8%; Pred. No. 5.4e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Mismatches
PRIOR APPLICATION NUMBER: FR 0205753
PRIOR FILING DATE: 2002-05-07
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
NUMBER OF EQ ID NOS: 162
SOFTWARE: PAEGNICH VET: 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 73, Application US/11012353
Publication No. US0050249730A1
GENERAL INFORMATION:
APPLICANT: GOETSCH, LILIANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 82.88
Matches 96; Conservative
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; ORGANISM: Mus musculus
US-11-012-353-52
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Sequence 72, Application US/11012353
Publication No. US20050249730A1
GENERAL INFORMATION:
APPLICANT: GORTSCH, LILIANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: BECEK, OLIVIER
APPLICANT: BECEK, ALAIN
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Best Local Similarity 79.0%;
Matches 98; Conservative
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US-11-054-515-1548
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61 KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARY-----GRVF-FDYWGQGTLV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLQESGPGLVKPSETLSLTCTVSNYSISSGYYWGWIRQPPGKGLEWIGSIYYSGSTYY 60
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Sequence 1651, Application US/11054515

Publication No. US2005025532A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523P3

CURRENT APPLICATION NUMBER: US/11/054,515

CURRENT FILING DATE: 2005-02-10

PRIOR APPLICATION NUMBER: 60/503,326

PRIOR APPLICATION NUMBER: 60/503,347

PRIOR APPLICATION NUMBER: 10/293,418

PRIOR PILING DATE: 2004-06-18

PRIOR PILING DATE: 2001-11-14

PRIOR PILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR PILING DATE: 2001-11-16

PRIOR PILING DATE: 2001-12-19

PRIOR PILING DATE: 2001-01-25

PRIOR PILING DATE: 2001-05-25

PRIOR PILING DATE: 2001-05-25

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16
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NUMBER OF SEQ ID NOS: 3247
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Sequence 1548, Application US/11054515
PUblication No. US2005025532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS; CURRENT APPLICATION UNBER: US/11/054,515
CURRENT APPLICATION UNBER: US/11/054,515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.6%; Score 491.5; DB 7; Length 247; 79.0%; Pred. No. 1.8e-36; Live 4; Mismatches 15; Indels 7
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Best Local Similarity 79.0
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
CORGANISM: Homo sapiens
US-11-054-515-1651
                                                                                  114 TVSS 117
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61 NPSLKSRVTISVDTSKNQPSLKLSSVTAADTAVYYCARVHYDILTGYLWAFDIWGQGTMV 120
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TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-198
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT PILING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: F00735,916
PRIOR APPLICATION NUMBER: F7 0308538
PRIOR FILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: FR 020553
PRIOR FILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-01-10
PRIOR FILING DATE: 2003-01-10
PRIOR FILING DATE: 2003-01-10
PRIOR FILING DATE: 2002-05-07
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
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PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR PLILAG DATE: 2004-02-11
PRIOR PLILAG DATE: 2004-06-18
PRIOR PLILAG DATE: 20014-06-18
PRIOR PLING DATE: 2001-11-14
PRIOR PLILAG DATE: 2001-11-14
PRIOR PLILAG DATE: 2001-11-16
PRIOR PLILAG DATE: 2001-11-16
PRIOR PLILAG DATE: 2001-12-19
PRIOR PLILAG DATE: 2001-12-19
PRIOR PLILAG DATE: 2001-06-15
PRIOR PLILAG DATE: 2001-06-15
PRIOR PLILAG DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/29, 499
PRIOR PLILAG DATE: 2001-03-26
PRIOR PLILAG DATE: 2001-03-16
PRIOR PLILAG DATE: 2001-03-16
PRIOR PLILAG DATE: 2001-03-16
PRIOR PLILAG DATE: 2001-03-16
PRIOR PLING DATE: 2001-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
PLINGTON DATE: 200
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Pred. No. 1.9e-36;
5; Mismatches 14; Indels 7
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US-10-721-763-17
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Fublication No. US2005025532A1
GENERAL INFORMATION:
TILL OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REPRENCE: PF5237E.
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT APPLICATION NUMBER: 60/543,296
FRIOR PELING DATE: 2004-02-11
FRIOR APPLICATION NUMBER: 60/543,296
FRIOR PELING DATE: 2004-02-11
FRIOR APPLICATION NUMBER: 60/540,347
FRIOR PELING DATE: 2004-06-18
FRIOR PELING DATE: 2001-11-16
FRIOR PELING DATE: 2001-11-16
FRIOR PELING DATE: 2001-11-16
FRIOR PELING DATE: 2001-12-19
FRIOR PELING DATE: 2001-01-2-19
FRIOR PELING DATE: 2001-03-21
FRIOR PELING DATE: 2001-03-21
FRIOR PELING DATE: 2001-03-21
FRIOR PELING DATE: 2001-03-16
FRIOR FILING DATE: 2001-03-17
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Best Local Similarity 77.2%; Pred. No. 1.3e-35;
Matches 98; Conservative 6; Mismatches 13; Indels 10; Gaps
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SEQ ID NO 1619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 7; Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 483; DB 7; Length 11
Pred. No. 5e-36;
5; Mismatches 17; Indels
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Best Local Similarity 81.2%;
Matches 95; Conservative
NUMBER OF SEQ ID NOS: 162
SOFTWARE: Patentin Ver. 3.3
SEQ ID NO 72
LENGTH: 117
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US-11-054-515-1619
                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                    FEATURE
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60 YKPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR-----YGRVF---FDYMGQG 110

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Db 61 YNPSLKSRVTISIDTSRNQFSLKLSSYTAADTAVYCVRSYYDILTGRPYTDAPDINGKG 120

QY 111 TLYTYSS 117

Db 121 TLYTYSS 127

185940re 17, Application US/10721763

19640re 17, Application US/10721763

19640re 17, Application US/10721763

19640re 17, Application WALTON

19640re 17, Application US/10721763

19640re 17, Application NOWINGER CONTROLL RANTIBODY

19640re 17, Application NOWINGER US/10/721,763

19640re 17, Application US/10/721,763
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Query Match
Best Local Similarity 85.0
Matches 102; Conservative
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MOLECULE TYPE: protein
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                                       Sequence 145, App
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Sequence 6, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 817, Appli
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625
1 QVQLQESGPGLVKPSETLSL......RYGRVFFDYWGQGTLVTVSS 117
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/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RR_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RR_COMB.pep:*
                     GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd
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US-09-490-070A-39
US-09-490-070A-39
US-09-490-153-39
US-09-490-153-65
US-09-490-324-65
US-09-490-324-65
US-09-30-613A-13
US-09-720-493-2
US-09-730-613A-13
US-09-490-153-25
US-09-490-153-25
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US-09-138-091A-77
US-09-138-091A-17
US-09-330-613A-17
US-09-330-613A-17
US-09-330-613A-17
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US-10-330-613A-9
US-09-471-276-837
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                                                                                                                                                                                                                                                                                                                                                                                                          572060 segs, 82675679 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                              - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length
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Perfect score:
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29 4775 76.6 279 2 US-09-05-257-3 Sequence 3. Appl. 29 477 76.6 279 119 1 US-09-40-774-2 Sequence 3. Appl. 20 477 76.7 119 1 US-09-40-775-2 Sequence 5. Appl. 20 476 76.2 119 1 US-09-40-775-2 Sequence 5. Appl. 20 476 76.2 119 1 US-09-40-75-2 Sequence 5. Appl. 20 476 76.2 119 1 US-09-40-75-2 Sequence 5. Appl. 20 476 76.2 119 1 US-09-40-75-2 Sequence 5. Appl. 20 476 76.2 119 1 US-09-40-5 Sequence 5. Appl. 20 475 76.1 122 1 US-09-40-5 Sequence 5. Appl. 20 475 76.2 119 1 US-09-40-5 Sequence 5. Appl. 20 475 76.2 119 2 US-09-40-5 Sequence 5. Appl. 20 475 76.1 122 1 US-09-40-5 Sequence 5. Appl. 20 475 76.1 122 1 US-09-40-5 Sequence 1. Appl. 20 475 76.1 122 1 US-09-40-5 Sequence 1. Appl. 20 475 76.1 122 1 US-09-40-5 Sequence 1. Appl. 20 475 76.1 122 1 US-09-40-5 Sequence 1. Appl. 20 475 76.1 122 1 US-09-40-5 Sequence 1. Appl. 20 475 76.1 122 1 US-09-40-5 Sequence 1. Appl. 20 475 76.1 122 1 US-09-40-5 Sequence 1. Appl. 20 475 76.1 122 1 US-09-40-5 Sequence 1. Appl. 20 475 76.1 122 1 US-09-40-5 Sequence 1. Appl. 20 47 75.8 122 1 US-09-40-5 Sequence 1. Appl. 20 47 75.8 122 1 US-09-40-5 Sequence 1. Appl. 20 47 75.8 122 1 US-09-40-5 Sequence 1. Appl. 20 47 75.8 122 1 US-09-40-5 Sequence 1. Appl. 20 47 75.8 122 1 US-09-40-5 Sequence 1. Appl. 20 47 75.8 122 1 US-09-40-5 Sequence 1. Appl. 20 47 75.8 122 1 US-09-40-5 Sequence 1. Appl. 20 47 75.8 122 1 US-09-40-5 Sequence 1. Appl. 20 47 75.8 122 1 US-09-40-5 Sequence 1. Appl. 20 47 75.8 122 1 US-09-40-5 Sequence 1. Appl. 20 47 75.8 122 1 US-09-40-5 Sequence 1. Appl. 20 47 75.8 122 1 US-09-40-5 Sequence 1. Appl. 20 47 75.8 122 1 US-09-40-5 Sequence 1. Appl. 20 47 75.8 122 1 US-09-40-5 Sequence 1. Appl. 20 47 75.8 122 1 US-09-40-5 Sequence 1. Appl. 20 47 75.8 122 1 US-09-40-5 Sequence 1. Appl. 20 47 75.8 122 1 US-09-40-5 Sequence 1. Appl. 20 47 75.8 122 1 US-09-40-5 Sequence 1. Appl. 20 47 75.8 122 1 US-09-40-5 Sequence 1. Appl. 20 47 75.8 122 1 US-09-40-5 Sequence 1. Appl. 20 47 75.8 122 1 US-09-40-5 Sequence 1. Appl. 20 47 75.8 122 1 US-09-40-5 Sequence 1. Appl. 20 47 75.8 122 1
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GENERAL INFORMATION:
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                                                                                                                                                                                    61 KPSLKDRVTISVDTSKNOFSLKLSSVTAADTAVYYCARYGRVFF---DYWGQGTLVTVSS 117
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                                                                                QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGYIYYSGSTNY 59
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                                      QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
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ZIP: 10021

ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: F10py disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., ESQ.
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
TELECOMMUNICATION INFORMATION:
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Pred. No. 2.8e-43;
3; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             \rm E:\ James\ F.\ Haley,\ Jr.,\ Esq.\ c/o\ Fish\ \&\ Neave\ 1251\ Avenue\ of\ the\ Americas
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 65, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: 11ag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.6%;
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Best Local Similarity 85.09
Matches 102; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                            US-09-025-769B-65
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; Sequence 39, Application US/09490070A; Patent No. 6696248

US-09-490-070A-39

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61 KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRVFF---DYWGQGTLVTVSS 117
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REDUM TYPE: PLOPBY disk

COMPUTER: IN PC compatible

COPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,070A

FILING DATE: 24-361-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-ANG-1995

ATONRY/AGENT INFORMATION:

NAME: Colin G. Sandercock, EBq.

REGISTATION NUMBER: 31,298

RESTERATION NUMBER: 31,298

REFERENCE/DOCKET NUMBER: 31,298

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
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Moroney, Simon
Plucckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSE: Colin G. Sandercock, Egg. c/o Heller Ehrman
                                                                                                         Moroney, Simon
Plucokthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 119;
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85.0%; Pred. No. 2.8e-43;
tive 3; Mismatches 11.
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-490-070A-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: <Unknown>
APPLICANT: Knappik, Achim
Pack, Peter
Ilaq, Vic
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Pack, Peter
Ilag, Vic
                                                                                   Ge, Liming
                                                                                                                                                                                                                                                                                                                        CITY: Washington STATE: D.C.
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Best Local Similarity 85.0
Matches 102; Conservative
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                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
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COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/S
FILING DATE: 24-Jan-2000 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGH: 119 amino acida
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10021
COMPUTER READABLE FORM:
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Best Local Similarity 85.0
Matches 102; Conservative
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US-09-490-153-65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLQESGPGLVXPSETLSITCTVSGGSIS-SYYWSWIRQPPGKGLEWIGXIXYSGSTNY 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Gaps
                                                                                                                  COMPUTER READABLE COMPUTER READABLE COMPUTER PROPRY disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/POCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acide
TWDE: amino acide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
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Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                            STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 510; DB 2;
Pred. No. 2.8e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
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APPLICATION NUMBER: US/09/490,153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
      White & McAuliffe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 39, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
                                                                                                            ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81.6%;
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STATE: New York
COUNTRY: USA
                                                CITY: Washington
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Best Local Similarity 85.0
Matches 102; Conservative
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61 KPSLKDRVTISVDISKNOFSLKLSSVTAADTAVYYCARYGRVFF---DYWGQGTLVTVSS 117
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; Sequence 65, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Knappik, Achim
; Ilag, Vic
Ge, Liming
Moroney, Simon
; Housekthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 510; DB 2;
Pred. No. 2.8e-43;
3; Mismatches 11
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AuG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
TELECOMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: James F. Haley, Jr., Esq. STREET: 1251 Avenue of the Americas CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
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ELEFAX: (212) 596-9090
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Knappik, Achim
Pack, Peter
                                   81.6%;
85.0%;
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Best Local Similarity 85.0
Matches 102; Conservative
                                 Query Match
Best Local Similarity 85.0
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   Ilag, Vic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
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US-09-490-324-65
US-09-490-324-39
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                                                                                                                                                                                                                                                                                                                                                              KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRVFF---DYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                            59
                                                                                                                                                                                                                                                                                                               1 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGYIYYSGSTNY
                                                                                                                                                                                                                                                                                          1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                                                      4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBW PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
                                                                                                                                                                                                                  Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 510; DB 2; Length 11
Pred. No. 2.8e-43;
3; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATE:

APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-3an-2000
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REFERENCE/DOCKET NUMBER: 27,794
REFERENCE/DOCKET NUMBER: 27,794
REFERENCE/DOCKET NUMBER: 27,794
TELEPHONE: (212) 596-9000
TELEFON FOR SEQ 1D NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLGGY: linear
MOLECTLE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
                  TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
                                                  INFORMATION FOR SEQ ID NO: 65:
                                                                                                                                                                                                                Query Match
Best Local Similarity 85.0%;
Matches 102; Conservative
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61 KPSLKDRVTISVDTSKNOFSLKLSSVTAADTAVYYCARYGRVFF---DYWGQGTLVTVSS 117
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                                                                                                                                                                                                                                                                                                                              59
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                                                                                                                                                                                                                          1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
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                                                                                                                     Gaps
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COMPUTER: READABLE FORM:

COMPUTER: Floppy disk

COMPUTER: Floppy disk

COMPUTER: Ploppy 
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           Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.6%; Score 510; DB 2; Length 119; 85.0%; Pred. No. 2.8e-43;
                                                                                                                     11; Indels
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Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
Score 510; DB 2;
Pred. No. 2.8e-43;
3; Mismatches 11;
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NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-490-324-65
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Patent No. 6828422
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 119 amino acids
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61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGD-GFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New York
                                                                                                                         RESULT 11
US-09-025-769B-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-025-769B-25
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60 NPSLKSRVTISVDTSKNOFSLKLSSVTAADTAVXYCARWGGDGFYAMDYWGGTLVTVSS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY 60
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81.1%; Score 507; DB 2; Length 117;
Best Local Similarity 84.6%; Pred. No. 5.5e-43;
Matches 99; Conservative 2; Mismatches 16; Indels
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79.5%; Score 497; DB 2; Length 117;
Best Local Similarity 84.7%; Pred. No. 5.4e-42;
Matches 100; Conservative 3; Mismatches 13; Indels
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Sequence 13, Application US/10330613A

Patent No. 6924360

GENERAL INFORMATION:

APPLICANT: Gudas, Jean

TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN

FILE REFERENCE: ABGENIX.022A

CURRENT APPLICATION NUMBER: US/10/330,613A

CURRENT FILING DATE: 2002-12-26

PRIOR PILING DATE: 2001-12-18

NUMBER OF SEQ ID NOS: 90

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                    Sequence 2, Application US/09720493
; Patent No. 6827925
; GENERAL INFORMATION:
APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Williams, Andrew J
APPLICANT: Tempest, Philip R
APPLICANT: Tempest, Philip R
APPLICANT: Holtet, Thor L
APPLICANT: Holtet, Thor L
APPLICANT: Ackson, Helen
APPLICANT: Daramolal Olalekan
APPLICANT: Daramolal, Olalekan
APPLICANT: Daramolal, Olalekan
APPLICANT: Jackson, Helen
APPLICANT: Jackson, He
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ORGANISM: Homo sapiens
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LENGTH: 117
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1 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGEIYHSGSTNY 59
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                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:

ZIP: 10021
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC Compatible
COMPUTER: PatentIn Release #1.0, Version #1.30 (BPO)
SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-F8E1998
FILING DATE: 18-F046.1995
FILING DATE: 18-F046.1995
ATTORNEY/AGENT INPORMATION:
NAME: James F. Haley, Jr., Esq.
REFERENCE/DOCKET NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAND: (212)596-9000
TRUBERX: (212)596-9000
TRUBERX: (212)596-9000
TRUBERX: (212)596-9000
TRUBERX: (212)596-9000
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                                                                                                                                                                                                                                                                                  ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York
                                                                  APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
NUMBER OF SEQUENCES: 373
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Pred. No. 1.2e-41;
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Sequence 25, Application US/09025769B; Patent No. 6300064; GENERAL INFORMATION:
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Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
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Best Local Similarity 84.03
Matches 100; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS: ADDRESSE: James F. F
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Query Match
Best Local Similarity
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US-09-490-324-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 KPSLKDRVTISVDTSKNOFSLKLSSVTAADTAVYYCA--RYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGRGGGGVFDYWGQGTLVTVSS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                           COUNTRY: USER
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PLOPPY disk
COMPUTER: DOOS MS-DOS
SOFTWARE: PECHTIN Release #1.0, Version #1.30 (EPO)
SOFTWARE: PECHTIN RAPESE: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: US/09/490,070A
FILING DATE: 18-AUG-1995
ATTORNEY AGENT INFORMATION:
NAWE: COlin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
                                                                  ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McAuliffe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                               STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
79.0%; Score 493.5; DB 2
Best Local Similarity 84.0%; Pred. No. 1.2e-41;
Matches 100; Conservative 3; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 25, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10021
COMPUTER READABLE FORM:
                                                                                                                                     CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-490-070A-25
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US-09-490-153-25
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1 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGEIYHSGSTNY 59
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Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Pluckthun, Andreas
TITLE OF INVENTION: 973
CORRESPONDENCE ADDRESS:
ADDRESSER: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
COMPUTER: IBM PC_compatible
COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 118;
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                                                                                                                                                                                          APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F . Haley, Jr., Bsq.
REFERENCE/DOCKET NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
FELENGENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acide
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84.0%; Pred. No. 1.2e-41;
tive 3; Mismatches 13
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APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-PEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: «Unknown»;
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-153-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 25, Application US/09490324; Patent No. 6828422; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Pest Local Similarity 83.8%; Pred. No. 3.7e-41;
Matches 98; Conservative 7; Mismatches 9; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 79.0%; Score 493.5; DB 2; Length 118; Best Local Similarity 84.0%; Pred. No. 1.2e-41; Matches 100; Conservative 3; Mismatches 13; Indels 3
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REGISTRATION INCORPATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: <UNKNOWN>
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-324-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 79, Application US/08918148A
Patent No. 634220
GENERAL INFORMATION:
APPLICANT: Adams, Camellia
APPLICANT: W.
APPLICANT: Gerter, Paul J.
APPLICANT: Gerter, Paul J.
APPLICANT: Gerter, Paul J.
APPLICANT: Gerter, Paul J.
APPLICANT: Gurney, Austin L.
TITIE OF INVENTION: Agonist Antibodies
FILE REFERENCE: P0979
CURRENT APPLICATION NUMBER: US/08/918,148A
CURRENT FILING DATE: 1997-08-25
NUMBER OF SEQ ID NOS: 79
IENGTH: 244
TYPE: PRT
TYPE: PRT
USGANISM: artificial
US-08-918-148-79
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US-08-918-148-79
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Search completed: January 10, 2006, 20:58:05 Job time: 22.847 secs

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January 10, 2006, 20:07:41; Search time 80.7649 Seconds (without alignments) 636.505 Million cell updates/sec
                                                                                                                                                                                            1 QVQLQESGPGLVKPSETLSL......RYGRVFFDYWGQGTLVTVSS 117
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5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                              2443163 seqs, 439378781 residues
version :
- 2006 (
                                                                                                                                                                                                                                                                                                                                                                                          Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                              - protein search, using sw model
                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
GenCore (c) 1993
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genesequ2000s:*
genesequ2001s:*
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genesequ2003s:*
genesequ2003s:*
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Maximum DB seq length: 200000000
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625
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               Copyright
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                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                              Scoring table:
                                                              OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database :
                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                               Searched:
                                                                                             Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Adj76917 Anti-IGF-	Adz67087 Human ant	6	Adz67089 Human ant	Adj76913 Anti-IGF-	Adz67083 Human ant	Adj76915 Anti-IGF-	Adz67085 Human ant	Adj76909 Anti-IGF-	-	Adj76911 Anti-IGF-	-	Adj76903 Anti-IGF-	Adz67073 Murine im	Adj76886 Anti-IGF-		Aay15126 Anti-muri	Adp03973 Murine-ex	Ads16559 Human ant	Adc27457 Humanised	Adp03885 Murine-ex	Adp03889 Murine-ex	Adp03958 Murine-ex	Adp03957 Murine-ex
SUMMARIES	ΠD	ADJ76917	ADZ67087	ADJ76919	ADZ67089	ADJ76913	ADZ67083	ADJ76915	ADZ67085	ADJ76909	ADZ67079	ADJ76911	ADZ67081	ADJ76903	ADZ67073	ADJ76886	ADZ67056	AAY15126	ADP03973	ADS16559	ADC27457	ADP03885	ADP03889	ADP03958	ADP03957
	Length DB	117 7	117 9	135 7	135 9	117 7	117 9	135 7	135 9	117 7	117 9	135 7	135 9	117 7	117 9	127 7	127 9	246 3	119 7	121 8	120 7	122 7	122 7	120 7	116 7
de	Query	100.0	100.0	100.0	100.0	98.4	98.4	98.4	98.4	97.8	97.8	97.8	97.8	84.6	84.6	84.6	84.6	83.1	82.7	82.6	82.3	82.2	82.2	82.0	81.7
	Score	625	625	625	625	615	615	615	615	611	611	611	611	529	529	529	529	519.5	517	516.5	514.5	513.5	513.5	512.5	510.5
	Result No.	-	7	е	4	Ŋ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24

Adio 5658 Human ant Adio 2658 Human ant Adp03884 Murine-ex Adp03884 Murine-ex Adw27554 Human Ab Abil 8676 Antibody Ady74798 Human ant Ady44615 Human ant Ade28455 Human ant Ade28459 Human ant Ade28456 Human ant Ade28456 Human ant Ade28456 Human ant Ade28456 Human ant Ade289267 Human ant Ady398267 Human ant Ady398267 Human ant	
5 ABB07171 7 ADP03887 7 ADP03884 2 AAW27554 6 ABJ16676 6 ABJ16676 7 ADE28479 7 ADE28479 6 AA030915 6 AA030913 6 AA030913 9 AEA21456 9 ADX98267	A MASISOS B ADS16613 7 ADE28491 A MASO1828 7 ADX01828 9 ADX01838
121 1221 1222 1122 1119 1119 122 122 122	121 121 121 121 123 248
81.7 81.7 81.7 81.6 81.6 81.1 81.1 81.1 81.1 80.9	880 800.7. 800.66 800.57.
510.5 510.5 510.5 510.5 510.5 510.5 507 507 507 507 507 507 507 507 507	000 400 000 000 000 000 000 000 000 000
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

## ALIGNMENTS

cytostatic; antipsoriatic; antibody; idF-lR; tyrosine kinase activity; insulin-like growth factor-1 receptor; IGF-lR; tyrosine kinase activity; or epidermal growth factor sceptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region; (FABR ) FABRE MEDICAMENT SA PIERRE. ADJ76917 standard; protein; 117 AA Anti-IGF-1R related protein #26. Leger O; 18-JAN-2002; 2002FR-0000653. 18-JAN-2002; 2002FR-0000654. 07-MAY-2002; 2002FR-00005753. 20-JAN-2003; 2003WO-FR000178. 06-MAY-2004 (first entry) Corvaia N, WPI; 2003-569653/53. WO2003059951-A2. Homo sapiens. 24-JUL-2003. Goetsch L, ADJ76917; RESULT 1 ADJ76917 

New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.

Disclosure; SEQ ID NO 83; 164pp; French

The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of

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             transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; heavy chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
                                                                                                                                                                                                                                                                                                KPSLKDRVTISVDTSKNQPSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                 KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                    QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                             QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human antibody 7C10 3 heavy chain variable region SEQ ID NO:83.
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                                                                                                                                                                  Length 117;
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receptors with their ligands. Especially they inhibit
                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haeuw J,
                                                                                                                                                             100.0%; Score 625; DB 7;
100.0%; Pred. No. 1.9e-49;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leger O,
                                                                                                                                                                                                                                                                                                                                                                                                               ADZ67087 standard; protein; 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003MO-FR001178.
11-JUL-2003; 2003FR-00008538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-DEC-2003; 2003US-00735916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                               Matches 117; Conservative
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                                                                                                                                                             Query Match
Best Local Similarity
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CORVAIA N.
LEGER O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DUFLOS A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAEUW J.
                                                                                                                                 Sequence 117 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JUN-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                               ADZ67087;
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(LEGE/)
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(HAEU/)
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The invention relates to a novel isolated anti-insulin-like growth factor capable of binding to human IGF-IR and, if necessary, capable of capable of binding to human IGF-IR and, if necessary, capable of capable of binding to human IGF-IR and, if necessary, capable of capable of binding to human IGF-IR and, if necessary, capable of capable of pecifically inhibiting tyrosine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal cativation of the IGF-IR and/or connected with a chyperactivation of the IGF-IR and/or connected with a chyperactivation of the medicament does not induce or only glightly induces secondary effects connected with inhibition of the insulin cereptor. The antibody is useful for preparation of a medicament intended co inhibit the transformation of normal cells into cells with tumoral chemanacter, preferably IGF-dependent, especially IGF-dependent and/or IGF2-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent cells, preferably IGF-dependent cells, in the preparation of a medicament intended for the treatment of cancer, where the cancer is chosen from prostate cancer, osteosarcoma, lung cancer, the cancer is chosen from prostate cancer, osteosarcoma, lung cancer, the cancer is chosen from prostate cancer, osteosarcoma, lung cancer, cells expressing or overexpressing the IGF-IR and/or EGF receptor.

CE breat cancer, andometrial cancer or colon cancer. (I) is useful in the preparation of a medicament intended for the specific targeting of a biologically which is optionally labeled. The present cells useful in which the abnormal presence, of IGF-IR and/or EGF receptor IS useful in the exemplifica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inaulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-IGF-1R related protein #27.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-MAY-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003059951-A2.
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69. .84 /note= "CDR2" 117. .124 /note= "CDR3"

2002FR-00000653

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18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WO-FR000178.
11-JUL-2003; 2003FR-00008538.
                                                                                                                                                          16-DEC-2003; 2003US-00735916
                                                                                      US2005084906-A1
                                                                                                                                                                                              8-JAN-2002;
                                                                                                                          21-APR-2005.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Goetsch L,
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(HAEU/)
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                                                                                                                                                                                                                                                                                                                            CORV/)
                                                                                                                                                                                                                                                                                                                                             LEGE/)
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                                                                                                                                                                                                                                                                                                    The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or rear diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate. I ung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gymecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79 KPSLKDRVTISVDTSKNQPSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                 New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 625; DB 7; Length 135; 100.0%; Pred. No. 2.2e-49; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein sequence used to generate the Ab of the invention
                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 85; 164pp; French.
                                                                                                       (FABR ) FABRE MEDICAMENT SA PIERRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADZ67089 standard; protein; 135 AA
                                                    18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-00005753.
 20-JAN-2003; 2003WO-FR000178.
                                   18-JAN-2002; 2002FR-00000653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JUN-2005 (first entry)
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Matches 117; Conservative
                                                                                                                                             Corvaia N,
                                                                                                                                                                             WPI; 2003-569653/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 135 AA;
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Beck A;

Duflos A, Haeuw J,

Leger O,

Corvaia N,

BECK A.

GOETSCH L. CORVAIA N. LEGER O. DUFLOS A. HAEUW J.

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The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting to human IGF-IR and, if necessary, capable of specifically inhibiting to human IGF-IR and, if necessary, capable of specifically inhibiting to be an interest on complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful interaction of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or connected with a creativation of the IGF-IR and/or EGFR, and/or connected with an intended or interaction of the intended or interaction of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin creaptor. The antibody is useful for preparation of a medicament intended control of induces accordary effects connected with inhibition of the insulin creaptor. The antibody is useful for preparation of a medicament intended control of a medicament intended to inhibit the transformation of normal cells into cells with tumoral capacitally IGF1-and/or IGF2-dependent and/or EGF2-dependent and/or IGF2-dependent and/or EGF2-dependent and/or IGF2-dependent of a medicament intended for prevention or toor the present of a medicament int
                                                                                                      Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
                                                                                                                                                                                                                                                                                                                                                                                            Example 13; SEQ ID NO 85; 125pp; English.
                                                                                                                                                                                                                                                                                     useful for treating cancer
WPI; 2005-321968/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 135 AA
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/note= "leader peptide" Location/Qualifiers

Homo sapiens

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ò 셤 8 Peptide Region

/note= "CDR1"

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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF) and/or -2; and/or (ii) inhibit specifically tyrosine (Kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit crowth and/or formal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and prostate, lung, breast, andometrium and colon, also osteosarcoma, and by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                      cytostatic, antipsoriatic, antibody; IGF-1R; tyrosine kinase activity; insulin-like growth factor-1 receptor; IGFR; signal transduction pathway; or epidermal growth factor receptor; NGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                             78
                                                                                                                                                KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                   growth factor receptor, of cancers.
                                                                                              QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                         QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                         Gaps
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0
Length 135;
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 Score 625; DB 9;
                  100.0%; Pred. No. 2.2e-49; ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 79; 164pp; French
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (FABR ) FABRE MEDICAMENT SA PIERRE.
                                                                                                                                                                                                                                                                           ADJ76913 standard; protein; 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leger 0;
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   100.001
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07-MAY-2002; 2002FR-00005753.
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                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                     117; Conservative
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   Query Match
Best Local Similarity
Matches 117; Conserv
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The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tyrosine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino the preparation of a medicament intended for the prevention for useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or connected with a activation of the transduction pathway of the signal mediated by the interaction of IGFP or IGF2 with IGF-IR and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly
                                                                                                                                                                                                                                                                                                     Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
                                                            KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                              QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
               antibody 7C10 2 heavy chain variable region SEQ ID NO:79.
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                                                                                                                                                                           ADZ67083 standard; protein; 117
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; 2002FR-00005753.
; 2003WO-FR000178.
; 2003FR-00008538.
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                                                                                                                                                                                                                                                                                                                                                                                                       chain variable region
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CORVAIA N.
LEGER O.
DUFLOS A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAEUW J.
BECK A.
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11-JUL-2003;
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(BECK/)
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ADZ67083
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Gaps

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Score 615; DB 7; Length 117; Pred. No. 1.6e-48; 1; Mismatches 1; Indels

Query Match 98.4%; Best Local Similarity 98.3%; Matches 115; Conservative

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induces secondary effects connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral character, preferably IGF-dependent, especially IGF1 and/or IGF2.

C dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is useful for preparation of a medicament intended to inhibit the growth and/or the probliferation of tumor cells, preferably IGF-dependent.

CC HER2/neu-dependent cells. (I) is useful in the preparation of a medicament intended for prevention or for the treatment of cancer, where the cancer is chosen from prostate cancer, osteosarcoma, lung cancer, breast cancer, edometrial cancer or colon cancer. (I) is useful in the preparation of a medicament intended for the prevention or for the treatment of psoriails. (I) is useful in preparation of a medicament cintended for the prevention of a medicament cintended for the prevention of a medicament cintended for the prevention of a medicament cintended for the specific targeting of a biologically active compound to cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I) is useful for in vitro diagnosis of illnesses induced by an expression of a medicament of the prevention of a medicament of proper in vitro diagnosis of illnesses induced by an expression of a medicament of the prevention of a medicament of the p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (1), which is optionally labeled. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytostatic; antipsoriatic; antibody; insulin-like growth factor-1 receptor; IGP-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antibodies that bind to human insulin-like growth factor receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 615; DB 9;
Pred. No. 1.6e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (FABR ) FABRE MEDICAMENT SA PIERRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADJ76915 standard; protein; 135 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-IGF-1R related protein #25.
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18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-00005753.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 98.3%;
Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-569653/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 117 AA;
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fragments, that bind to human insulan-like growth factor-1 receptor (IGF-1R) and optionally: (1) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (11) inhibit specifically tyrosine kinase activity of IGF-1R. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or or pidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human antibody 7C10 2 heavy chain variable region SEQ ID NO:81.
                                                                                                                                                                                                                                                                                                                                                                         Score 615; DB 7; Length 135;
Pred. No. 1.8e-48;
1; Mismatches 1; Indels
useful for treatment, prevention and diagnosis of cancers
                                                                 (Ab)
                                                                 invention relates to an isolated antibody
                                   Disclosure; SEQ ID NO 81; 164pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .18
'note= "leader peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADZ67085 standard; protein; 135 AA
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/note= "CDR2"
117. .124
/note= "CDR3"
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/note= "CDR1"
                                                                                                                                                                                                                                                                                                                                                                       98.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUN-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                            Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                          Sequence 135 AA;
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ADJ76909 standard; protein; 117 AA.

RESULT 9 ADJ76909 Anti-IGF-1R related protein #22.

06-MAY-2004 (first entry)

ADJ76909;

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Ire invention included violation is the functional fragment, being capable of binding to human igF-TR and, if necessary, capable of specifically inhibiting to human igF-TR and, if necessary, capable of specifically inhibiting tyroshie kinase activity of the receptor, comprising a light or heavy chain having at least one complementary capable of specifically inhibiting tyroshie have a city with one determining region (CDR) consisting of one of two fully defined is amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in cariation of a medicament intended for the prevention or treatment of an intense connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGPR, and/or connected with a crivation of the IGF-IR and/or EGPR, and/or connected with a chiperaction of the IGF-IR and/or of EGF with EGPR, where the administration of the medicament does not induce or only slightly induced interaction of the medicament does not induce or only slightly receptor. The antibody is useful for preparation of a medicament intended condition of two inhibit the transformation of normal cells into cells with tumoral character, preferably IGF-dependent and/or HERZ/hou-dependent and/or IGF2-dependent and/or IGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel isolated anti-insulin-like growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         Beck A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         Haeuw J,
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Pred. No. 1.8e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                     Duflos A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 13; SEQ ID NO 81; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                         Leger O,
                               20-JAN-2003; 2003WO-FR000178.
11-JUL-2003; 2003FR-00008538.
07-MAY-2002; 2002FR-00005753.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 98.3
Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         Corvaia N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2005-321968/33.
                                                                                                                                             GOETSCH L.
CORVAIA N.
LEGER O.
DUFLOS A.
HAEUW J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ADZ67084
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                                                                                                                                                                                                                                                                                                                                              BECK A.
                                                                                                                                                                                                                                                                                                                                                                                                                         Goetsch L,
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(HAEU/)
(BECK/)
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(LEGE/)
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Query Match
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                                                                                                                                            61 KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                        QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                         19 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                               98.3%; Pred. No. 1...
98.3%; Pred. No. 1...
1; Mismatches
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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or recet diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of transformation of tumor cells, so are useful against cancers of the profiteration of tumor cells, so are useful against cancers of the profiter and parality paorianis. Bapecially they inhibit growth and/or proliferation of tumor cells, and also osteosarcoma, and also for treating psorianis. Ab are a lso used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                             cytostatic; antipsoriatic; antibody; insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 KPSLKDRVTISVDTSKNOFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein sequence used to generate the Ab of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 3.7e
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 75; 164pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (FABR ) FABRE MEDICAMENT SA PIERRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leger 0;
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18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-0005753.
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Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corvaia N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-569653/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 117 AA;
                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                      24-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goetsch L,
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The invention relates to a novel isolated anti-institution of the invention relates to a novel isolated anti-institution being capable of capable of binding to human IGF-IR and, if necessary, capable of capable of binding to human IGF-IR and, if necessary, capable of capable of binding to human IGF-IR and, if necessary, capable of capable of binding to human IGF-IR and, if necessary, capable of capable of ADZ67004 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal contivation of the IGF-IR and/or EGFR, and/or connected with a chyperactivation of the IGF-IR and/or EGFR, and/or of EGF with EGFR, where interaction of IGF-IR and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin creeptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral character, preferably IGF-dependent and/or IGF2 and/or IGF2-dependent and/or EGF-dependent and/or IGF2-dependent and/or IGF2
                                                                                                                                                                                                                                                                                                                                                  Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; prosplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskoletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel isolated anti-insulin-like growth factor
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                                                                                                                                                                                                                                                                  Human antibody 7C10 1 heavy chain variable region SEQ ID NO:75.
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ADZ67079 standard; protein; 117 AA
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2002FR-00000654.
2002FR-00005753.
2003WO-FR000178.
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                                                                                                                                                                         (first entry)
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CORVAIA N.
LEGER O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DUFLOS A. HAEUW J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2005084906-A1.
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20-JAN-2003;
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(LEGE/)
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(HAEU/)
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preparation of a medicament intended for the prevention or for the treatment of psoriasis. (I) is useful in preparation of a medicament intended for the specific targeting of a biologically active compound to cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I) is useful for in vitro diagnosis of illnesses induced by an overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (I), which is optionally labeled. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-1R) and optionally: (1) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (1) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region; CDR.
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                                                                                                                                                                                                                                                                                                                                                                                      61 KPSLKDRVTISVDTSKNOFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                                                                                                                                                  QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                        Length 117;
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                                                                                                                                                                                                                                        97.8%; Score 611; DB 9; 96.6%; Pred. No. 3.7e-48; ive 3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 77; 164pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic; antipsoriatic; antibody;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADJ76911 standard; protein; 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-IGF-1R related protein #23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JAN-2002; 2002FR-0000654
07-MAY-2002; 2002FR-00005753
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                                                                                                                                                                                                                                                            dest Local Similarity 96.0
Atches 113; Conservative
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                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                          Sequence 117 AA;
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WPI; 2005-321968/33. N-PSDB; ADZ67080.

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      transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                             neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; heavy chain variable region.
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                                                                                                                                                                      KPSLKDRVTISVDTSKNOFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
                                                                                                                                 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                 Human antibody 7C10 1 heavy chain variable region SEQ ID NO:77.
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receptors with their ligands. Especially they inhibit
                                                                                            Length 135;
                                                                                                               1; Indels
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                                                                                             Score 611; DB 7;
Pred. No. 4.3e-48;
                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   "leader peptide"
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/note= "CDR2"
117. .124
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/note= "CDR1"
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'note= "CDR3"
                                                                                            97.8%;
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2002FR-00005753.
2003WO-FR000178.
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                                                                                                               Matches 113; Conservative
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                                                                                                      Local Similarity
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CORVAIA N.
LEGER O.
DUFLOS A.
HAEUW J.
                                                                          Sequence 135 AA;
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                                                                                                                                                                                                                                                            ADZ67081;
                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
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Transcription (1967-IR) antibody (1) or its functional fragment, being grown in invention fragues of binding to human IGF-IR and, if necessary, capable of appable of binding to human IGF-IR and, if necessary, capable of appable of binding to human IGF-IR and, if necessary, capable of appable of binding to human IGF-IR and, if necessary, capable of appable in the prediction of binding typosise in the comprising a light or heavy chain having at least one complementary comprising a light or heavy chain having at least one complementary cards (ADZ67006 and ADZ67014). An antibody of the invention is useful in cardia (ADZ67006 and ADZ67014). An antibody of the prevention or treatment of an illuses connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or connected with a critication of the IGF-IR and/or EGFR, and/or connected with a critication of the medicament does not induces accordary effects connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral caparation of a medicament intended to inhibit the growth and/or EGF-dependent and/or EGF-dependent and/or IGF2-dependent cells, preferably IGF-dependent and/or IGF2-dependent cells, (I) is useful in the preparation of a medicament intended for prevention or for the treatment of partial cancer, colorated partial ander and/or IGF2-dependent cells, (I) is useful in preparation of a medicament intended for prevention or for the preparation of a medicament intended for the prevention or color the preparation of a medicament intended for the prevention or color the preparation of a medicament intended for the prevention or color the prevention or color and prevention or color ander (I) is useful in the preparation of a medicament intende
                                                                                                                                                                                                                                                                                                      The invention relates to a novel isolated anti-insulin-like growth factor
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Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
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Pred. No. 4.3e-48;
3; Mismatches 1; Indels
                                                                                                                                                                                                                 Example 13; SEQ ID NO 77; 125pp; English.
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Matches 113; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (IGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; copplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNYK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; BGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunoglobulin heavy chain variable region 7C10 VH SEQ ID NO:69
                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 PSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 PSLKDRISITRDISKNQFFLKLNSVTNEDTATYYCARYGRVFFDYWGQGTTLIVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84.6%; Score 529; DB 7; Length 11
82.8%; Pred. No. 1.2e-40;
ive 11; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 69; 164pp; French
                                                                                                                                                                                                                                                                                                                                          (FABR ) FABRE MEDICAMENT SA PIERRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADZ67073 standard; protein; 117 AA
                                                                                                                                                                                                                                                                                                                                                                                  Leger 0;
                                                                                                                                                                                                                                                                                  18-JAN-2002; 2002FR-0000654. 07-MAY-2002; 2002FR-00005753.
                                                                                                                                                                                                                                                             18-JAN-2002; 2002FR-00000653.
                                                                                                                                                                                                                       20-JAN-2003; 2003WO-FR000178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 82.8
hes 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    Goetsch L, Corvaia N,
                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-569653/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 117 AA;
                                                                                                                                        WO2003059951-A2
                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUN-2005
                                                                                                                                                                               24-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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      XXX5X6X5X8
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The invention relates to a novel isolated anti-insulin-like growth factor

I receptor (IGF-IR) antibody (I) or its functional fragment, being

compatible of binding to human IGF-IR and; if necessary, capable of

specifically inhibiting tyrosline kinase activity of the receptor,

comprising a light or heavy chain having at least one complementary

determining region (CDR) consisting of one of two fully defined 16 amino

acids (ADZ67016 and ADZ67014). An antibody of the invention is useful in

confer segion (CDR) consisting of one of two fully defined 16 amino

acids (ADZ67016 and ADZ67014). An antibody of the invention is useful in

confer includes connected with an overexpression and/or an abnormal

activation of the IGF-IR and/or EGFR, and/or connected with a

confirmation of the IGF-IR and/or EGFR, and/or connected with a

interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where

continues accondary effects connected with inhibition of the insulant

induces secondary effects connected with inhibition of the insulant

contacter, preferably IGF-dependent, especially IGF1 and/or IGF2-

consecut for preparation of a medicament intended to inhibit the transformation of medicament intended for prevention or the proparation of a medicament intended for prevention or the preparation of a medicament intended for prevention or the preparation of a medicament intended for prevention or to the treatment of cancer, endometrial cancer or colon cancer. (I) is useful in the preparation of a medicament intended for prevention or colon cancer. (I) especially IGF1-and/or IGF2-dependent and/or EGF resement of proparation of a medicament intended for the specific targeting of a biologically active compount to reatment of parametrial cancer or colon cancer. (I) is useful in the preparation of a medicament intended for the specific targeting of a biologically active compount to reatment of parametrial cancer, endometrial cancer, cancer cancer, endometrial cancer cancer cancer cancer is chosen from prostate cancer canc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; immunoglobulin; heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beck A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haeuw J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Duflos A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 13; SEQ ID NO 69; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leger O,
                                                                                                                                                                                                                                                            18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WO-FR000178.
11-JUL-2003; 2003FR-00008538.
                                                                                                                                                                                                    16-DEC-2003; 2003US-00735916
                                                                                                                                                                                                                                         2002FR-00000653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corvaia N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2005-321968/33.
                                                                                                                                                                                                                                                                                                                                                          GOETSCH L.
CORVAIA N.
LEGER O.
                                                                                                                                                                                                                                                                                                                                                                                                                         DUFLOS A. HAEUW J.
                                                                                                                    US2005084906-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                BECK A.
                                                                                 Mus musculus.
                                                                                                                                                                                                                                           18-JAN-2002;
                                                                                                                                                            21-APR-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BECK/)
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                                                                                                                                                                                                                                                                                                                                                                                   CORV/)
                                                                                                                                                                                                                                                                                                                                                                                                        LEGE/
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Sequence 117 AA;

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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (1) inhibit matural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (1i) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or pidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit growth and/or proliferation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the proliferation of tumor cells, so are useful against cancers of the proliferation of cumor cells, and one prostocate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating pseciasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          insulin-like growth factor-1 receptor; IGP-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                   VOLOESGPGLVKPSOSLSLTCSVTGYSITGGYLMNMIROFPGNKLEWMGYISYDGTNNYK
                                                                           2 VOLOESGPGLUKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNYK
                                                                                                                                                                             PSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                        Gaps
                                        ö
  Length 117;
                                      9; Indels
Match 84.6%; Score 529; DB 9; Local Similarity 82.8%; Pred. No. 1.2e-40; les 96; Conservative 11; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 52; 164pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytostatic; antipsoriatic; antibody;
                                                                                                                                                                                                                                                                                               ADJ76886 standard; protein; 127 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (FABR ) FABRE MEDICAMENT SA PIERRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leger 0;
                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-IGF-1R related protein #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JAN-2002; 2002FR-0000653.
18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-0005753.
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                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003059951-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JUL-2003.
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Query Match
                                        Matches
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Length 127;

Score 529; DB 7; Pred. No. 1.3e-40;

84.6%;

Query Match Best Local Similarity

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                                  61
                                                           12 VQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNYK 71
                                2 VQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNYK
                                                                                                 PSLKDRVTISVDTSKNQPSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                72 PSLKDRISITRDTSKNQFFLKLNSVTNEDTATYYCARYGRVFFDYWGQGTTLTVSS 127
 Gaps
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9; Indels
 11; Mismatches
 96; Conservative
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   Matches
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Search completed: January 10, 2006, 20:44:18 Job time : 81.7649 secs

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GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd
                 Copyright
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- protein search, using sw model OM protein January 10, 2006, 20:28:02; Search time 14.1157 Seconds (without alignments) 797.508 Million cell updates/sec Run on

QVQLQESGPGLVKPSETLSL.......RYGRVFFDYWGQGTLVTVSS 117 US-10-735-916A-83 625 1 QVQLQESGPGLVKPS1 Title: Perfect score: Sequence:

283416 segs, 96216763 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:\*
1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES 137782 S31690 S30530 S13519 S31511 \$24443 \$30534 \$31586 \$31512 \$78055 \$74113 \$44114 \$49045 \$78051 \$09711 \$47010 \$20780 \$24770 \$26340 \$12421 \$316921 \$31696 \$37200 \$26906 \$4125 \$30529 \$54906 Query Match Length DB 473.5 473.5 473.5 465.5 466.5 46 Score 519 504 491 488 478 Result Š

RESULT 2
S18500
IS heavy chain V region - human (fragment)
C; Species: Homo saplems (man)
C; Species: Homo saplems (man)
C; Species: Homo saplems (man)
C; Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999
C; Jaccession: 831690
R; Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A; Description: Mechanisms that generate human immunoglobulin diversity operate from the A; Reference number: 831685
A; Accession: 831690
A; Statuer: preliminary
A; Molecule type: mRNA
A; Residues: 1-130 <CUI>A; Residues: 1-130 <CUI
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Reywords: heterotetramer; immunoglobulin

Ig heavy chain pre Ig heavy chain V r	Ig heavy chain V r Ig heavy chain V r Ig heavy chain pre	Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r	Ig heavy chain V r Ig heavy chain V-I Ig mu chain - huma	Ig heavy chain V r Ig heavy chain - h	Ig heavy chain V r Ig V-D-J region (N Ig heavy chain pre
B26340 S07637	S26902 S19668 AVMS35	S12416 S38718 S26802	S26803 B49028 S37456	128195 S31514	S26801 S69912 A41287
0 0	777	000	0 0 0	0 0	000
116	98 127 137	97 116 99	99 143 116	117	99 122 139
71.0	70.9 70.9	70.6 70.6 70.3	70.3	70.1	69.8 69.8 8.8
443.5 443.5	4 4 4 4 4 4 4 2 3	441.5 441.5 439.5	439.5 439 438	438	436.5 436.5 436.5
30	3 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	35 37	3 8 8 6 0 8 6 0	41	44 45 5

## ALIGNMENTS

	RESULT 1	1
	Ig vari	Ig variable region (VDJ) (clone T23-9) - human (fragment)
-	C;Speci C;Date:	c;bpecies: nomo Bapiens (man) C;Date: 16-Feb-1996 #sequence revision 13-Mar-1997 #text_change 23-Jul-1999
	C; Acces	C;Accession: 137782; S25476
	R;Demai	R; Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.
	Proc. N	Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994 A. mitle. commerie divoreification in the heave chain variable region genes expressed by 1
	A; Refer	A; receipt outper : A36876; MUID: 94119917; PMIS290556
	A; Acces	A; Accession: 137782
	A;Statu	A; Status: preliminary
	A; Molec	A; Molecule type: mRNA
	A;Resid	A;Residues: 1-140 <res></res>
	A;Cross	A, Cross-references: UNIPARC: UP10000176E83; EMBL: X67906; NID: 933582; PIDN: CAA48104.1; PI
	C; Super	C; Superfamily: immunoglobulin V region; immunoglobulin homology
	F;46-12	F;46-128/Domain: immunoglobulin homology <1MM>
	Query	
	Best Match	Best Local Similarity 84.6%; Freq. No. 5.76-40; Matches 104; Conservative 3; Mismatches 8; Indels 8; Gaps 3;
	λõ	1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDSTNNY 60
	qa	20 QVQLQESGPGLVKPSETLSLTCTVSGCSIS-SYYMSWIRQPPGKGLEWIGYIYYSGSTNY 78
	ò	61 KPSLKDRVTISVDISKNQFSLKLSSVTPADTAVYYCARYGRVFFDYNGQGTLVT 114
	qq	79 NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARHNSSSWYGR-YFDYWGQGTLVY 137
	ò	115 VSS 117 
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us-10-735-916a-83.rpr

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Gaps

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Indels

13;

96

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CiSpecies: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: 831511
R;Chastagner, P:/ Benaison, C.; Theze, J.; Zouali, M.
Submitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA autc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Actus: mRNA
A;Molecule type: mRNA
A;Residues: 1-155 <CHLA>
A;Cross-references: UNIPARC:UPI00001160FF; EMBL:X69866; NID:g33094; PIDN:CAA49500.1; PIC
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;47-129/bomain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: S24443
A; Molecule type: mRNA
A; Residues: 1-118 a.JON.
A; Residues: 1-118 a.JON.
A; Cross-references: UNIPARC: UP10000115FE9; EMBL: X61650; NID: g37720; PIDN: CAA43831.1; PII
B; Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Title: By-pagsing immunization. Human antibodies from V-gene libraries displayed on pł
A;Reference number: S19663; MUID:92085276; PMID:1748994
                                                                                                                                                                                                            87 YNPSLKSRVIISVDISKNQPSLKLSSVTAADTAVYYCARPLLWFGEL-FDYWGQGTLVTV 145
                                                                                                                                                                                 60 YKPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR----YGRVFFDYWGQGTLVTV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRV--FFDY-----WGQGTLV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.Date: 22-Jan-1993 #Bequence_revision 22-Jan-1993 #text_change 20-Jun-2000 C.Accession: S24443; S19667 C.Accession: S24443; S19667 R.Jones, P.T. R.Jones, P.T. A.S. Submitted to the EMBL Data Library, October 1991 A.Reference number: S24442
                                                                                                                     27 QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGSIYYSGSTY
                                                                                           1 QVQLQESGPGLVKPSETLSLTCTVSGYSI-SGGYLWNWIRQPPGKGLEWIGYISYDGTNN
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Score 488; DB 2; Length 147;
Pred. No. 3.8e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 478; DB 2;
Pred. No. 3.2e-36;
                                           4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig heavy chain V region (VH4DJ) - human
78.1%;
81.1%;
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                                             99; Conservative
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A; Molecule type: mRNA
A; Residues: 1-55,57-118 <MAR>
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A; Accession: S31511
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C;Date: 22-Jan-1993 #seq
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Matches 97; Conserv
                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig heavy chain - human
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  Query Match
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                        Best Local
Matches 9
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If heavy chain V region precursor - human

C, Species: Homo sapiens (man)

C, Species: J5-Reb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C, Accession: S13519

N, Title: Limmunoglobulin variable heavy chain cDNA sequence from a patient with X-linked

A, Reference number: S13519; MUID:91187691; PMID:2011536

A, Accession: S13519

A, Residues: L-147 * ANDR.

A, Modecule type: mRNA

A, Modecule type: mRNA

A, Residues: L-147 * ANDR.

A, Residues: L-147 * ANDR.

C, Superfamily: immunoglobulin V region; immunoglobulin homology

C, Superfamily: immunoglobulin Nemology < IMM>

F, 41-125/Domain: immunoglobulin homology < IMM>
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                                                                                                                                                                                                                                 61 KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR-----YGRV--FFDYWGQGT 111
                                                                                                                                                                                                                                                         65 NPSLKSRVTISVDTSKNQPSLKLSSVTAADTAVYYCARGSSVLLWPGBLLYYFDYWGQGT 124
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                                                                                                                                                                6 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWSRQPPGKGLEWIGYIYYSGSTNY 64
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                                                Length 130;
                                                                                           10; Indels
                                             Score 504; DB 2;
Pred. No. 1.2e-38;
5; Mismatches 10
F;20-102/Domain: immunoglobulin homology <IMM>
                                             Query Match 80.6%;
Best Local Similarity 80.2%;
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        heavy chain V region - human
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nes 98; Conserv
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Best Local S:
Matches 98
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Gaps

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13; Indels

Length 155;

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R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto
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A; Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
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                                                                                                                                                                                                                                                             9 NPSLKSRVTMSVDTSKNQFSLKLSSVTAADTAVYYCARGGLGIRRGAFDIWGGGTMVTVS 138
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C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C;Accession: S78052; S23717
R;Harindranath, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig heavy chain - human
C,Species: Homo sapiens (man)
C,Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
                                                                                                                                       20 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPAGKGLEWIGRIYTSGSTNY
                                                                                                                                                                                                                                     61 KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYG----RVFFDYWGQGTLVTVS
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A;Accession: S23717
A;Molecule type: mRNA
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      7.3e-36;
Pred. No. 7.3e-
4; Mismatches
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      80.2%;
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Best Local Similarity 76.61
Matches 95; Conservative
                                      97; Conservative
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A; Molecule type: mRNA
A; Residues: 1-140 <HAR>
          Similarity
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      Best Local
Matches 9
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S31586

Ig heavy chain V region - human (fragment)

Ig heavy chain V region - human (fragment)

C;Species: Homo sapies (man)

C;Species: Homo sapies

C;Accession: S31586

B;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.

Submitted to the EMBL Data Library, June 1992

A;Reference number: S31585

A;Accession: S31586

A;Reference number: S31586

C;Status: preliminary

A;Residues: 1-139 <CUI>
A;Cross-references: UNIPARC:UPIO00011646E; EMBL:Z14196; NID:g30978; PIDN:CAA78565.1; PIC

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin
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                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                             Length 118;
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                                      C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75.8%; Score 473.5; DB 2; Length 74.6%; Pred. No. 6.8e-36; ive 4; Mismatches 16; Indels
                                                                                                                                                                                                                                            Indels
                                                                                                                                                                          Score 473.5; DB 2;
Pred. No. 6.1e-36;
5; Mismatches 16;
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          A;Cross-references: UNIPARC:UPI0000176B52; EMBL:X61650
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                                                                                                                                                                          Query Match
Best Local Similarity 79.8%;
Matches 95; Conservative
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Best Local Similarity 74.69
Matches 97; Conservative
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GQGTMVTVSS 130
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
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Ig heavy chain V region (anti-B cell autoantibody) - human (fragment)
Cispecies: Homo sapiens (man)
         C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-129 <HAW>
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens
C;Accession: S78055; S23720
R;Harindranath, N.
Submitted to the EMBL Data Library, August 1990
A;Reference number: S78051
A;Accession: S78055
A;Reference number: S78051
A;Reference number: S78051
A;Residues: 1-145 c+HAR.
A;Cross-references: UNIPARC:UPIO000115E8C; EMBL:X54445; NID:g37817; PIDN:CAA38312.1; PIL
R;Harindranath, N.; Goldfarb, I.S.; Ikemateu, H.; Burastero, S.E.; Wilder, R.L.; Notkine
Int. Immunol. 3, 865-875, 1991
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h patient.
A;Reference number: S23716; MUID:92031262; PMID:1718404
A;Accession: S23720
A;Rocieule type: mRNA
A;Residues: 18-115 c+HAW.
A;Residues: 18-115 c+HAW.
A;Residues: 18-115 c+HAW.
A;Cross-references: UNIPARC:UPIO001769D2; EMBL:X54445
A;Cross-references: UNIPARC:UPIO001769D2; EMBL:X54445
A;Cross-references: UNIPARC:UPIO001769D2; EMBL:X54445
A;Cross-references: UNIPARC:UPIO001769D2; EMBL:X5445
A;Cross-references:UNIPARC:UPIO001769D2; EMBL:X5445
A;Cross-references:UNIPARC:UPIO001769D2; EMBL:X5445
A;Cross-references:UNIPARC:UPIO001769D2; EMBL:X5445
A;Cross-references:UNIPARC:UPIO001769D2; EMBL:X5445
A;Cross-references:UNIPARC:UPIO001769D2; EMBL:X5445
A;Cross-references:UNIPARC:UPIO001769D2; EMBL:X5445
A;Cross-references:UNIPARC:UPIONOTION UNIPARC:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR-----YGR-VFFDYWGQ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                          1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
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                                                                                                                                                                                                                                                                                  11;
A,Cross-references: UNIPARC:UPI0000116417; EMBL:X54441
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-14/Domain: signal sequence (fragment) #status predicted <SIG>
F;15-140/Product: Ig heavy chain (fragment) #status predicted <MAT>
F;29-111/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                 Query Match 75.4%; Score 471.5; DB 2; Length Best Local Similarity 74.8%; Pred. No. 1.1e-35; Matches 95; Conservative 6; Mismatches 15; Indels
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74.2%; Pred. No. 1.7e-35;
ive 5; Mismatches 17
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S44113
Ig heavy chain V region - human
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95; Conserv
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Best Local S
Matches 95
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Cjaccession: S44113

K; Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994

A; Reference number: S44105

A; Reference number: S44105

A; Retension: S44113

A; Status: preliminary

A; Modecule type: DNA

A; Residues: 1-121 < HAW>
                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPARC:UP1000011662F; EMBL;Z31389; NID:g472967; PIDN:CAA83264.1; PI CS.Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin homology cikeywords: heterotetramer; immunoglobulin homology cIMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPARC:UP10000116619; EMBL;231579; NID:g472968; PIDN:CAA83451.1; PI CS:Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin homology < IMM>
F;15-98/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116
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C;Accession: S78051; S23716
C;Accession: S78051; S23716
Submitted to the EMBL Data Library, August 1990
A;Reference number: S78051
A;Accession: S78051
A;Accession: S78051
A;Accession: S78051
A;Readques: 1-135 <-HAR>
A;Readques: 1-135 <-HAR>
A;Cross-references: UNIPARC:UP10000115E87; EMBL:X54437; NID:g37814; PIDN:CAA38306.1; PID
B;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notking
Int: Immunol. 3, 865-875, 1991
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h patient.
A;Reference number: S23716; MUID:92031262; PMID:1718404
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C;Accession: A9045
R;Grillot-Courvalin, C.; Brouet, J.C.; Piller, F.; Rassenti, L.Z.; Labaume, S.; Silverma Bur. J. Immunol. 22, 1781-1788, 1992
Ry. J. Immunol. 22, 1781-1788, 1992
A;Ritler: An anti-B cell autoantibody from Wiskott-Aldrich syndrome which recognizes i blangerence number: A49045; MUID:92324290; PMID:1623923
A;Reference number: A49045
A;Reterence number: A1000113EDD; GB:S39381; NID:G250899; PIDN:AAB22441.1; PID: A;Residues: 1-140 cGRI>
A;Reterences: UNIPRKC:UPI000113EDD; GB:S39381; NID:G250899; PIDN:AAB22441.1; PID: A;Residues: extracted from NCBI backbone (NCBIN:108088)
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology < IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRV-----FFDYWGQGTLVTV 115
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Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
Accession: S78051; S23716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 QVQLQQWGAGLLKPSETLSLTCAVYGGSFS-GYYWSWIRQPPGKGLEWIGEINHSGSTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig heavy chain precursor V-D-J region (clone mAB 61VH) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .,
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14-135/Product: Ig heavy chain (fragment) #status predicted <MAT>
27-111/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 74.4%; Score 465; DB 2; Length 135; Best Local Similarity 77.2%; Pred. No. 4.1e-35; Matches 95; Conservative 4; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 74.6%; Score 466; DB 2; Length 140; Best Local Similarity 77.0%; Pred. No. 3.5e-35; Matches 94; Conservative 6; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: S23716
A;Rolecule type: mRNA
A;Residues: 13-111 - HAMA
A;Cross-references: UNIPARC:UPI00001769D5; EMBL:X54437
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-13/Pomain: signal sequence (fragment) #status predicted <SIC
F;14-135/Product: Ig heavy chain (fragment) #status predicted <B;27-111/Domain: immunoglobulin homology <IMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 SS 117
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Search completed: January 10, 2006, 20:55:16 Job time: 15:1157 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: January 10, 2006, 20:26:41; Search time 78.8731 Seconds (without alignments)
1046.577 Million cell updates/sec
Title: US-10-735-916A-83
Perfect score: 625
Sequence: 1 QVQLQESGPGLVKPSETLSL......RYGRVFFDYWGQGTLVTVSS 117

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Total number of hits satisfying chosen parameters: 2166443

2166443 seqs, 705528306 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : UniProt\_05.80:\* 1: uniprot\_sprot:\* 2: uniprot\_trembl:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

ion	homo sapien		homo sapien	homo sapien	homo sapien	nomo sapien	mus musculu	homo sapien	homo sapien	nomo sapien	homo sapien	nomo sapien	mus musculu	mus musculu	mus musculu	mus musculu	homo sapien	homo sapien	homo sapien	nomo sapien	nomo sapien	nomo sapien	nomo sapien	mus musculu	homo sapien	mns musculu	rattus norv	rattus norv	mus musculu	homo sapien	mus musculu
Description	09ul73 }		_	06gmx7 }	_	_	_	_	_	_	_	_	-	_	P01822	_	_	_	_	_	_	_	_	_	_	-		• •	_	_	P18531
QI	Q9UL73 HUMAN	OGGMX6 HUMAN	QGGMX1 HUMAN	Q6GMX7 HUMAN	095973 HUMAN	Q6P4I8 HUMAN	Q99M22_MOUSE	Q96EY0_HUMAN	072379 HUMAN	Q7Z374_HUMAN	Q86SX2_HUMAN	Q96KX8 HUMAN	Q6LBQ5 MOUSE	Q5U413_MOUSE	HV46_MOUSE	Q53VQ5_MOUSE	Q8WUX4 HUMAN	Q9BU10_HUMAN	OGGMX5_HUMAN	Q96AA6 HUMAN	HV2I_HUMAN	Q9BQB8 HUMAN	Q8IZD7 HUMAN	Q53VQ1_MOUSE	Q6NYH3_HUMAN	Q53VR7 MOUSE	Q569B6_RAT	Q569B8_RAT	Q53VR3 MOUSE	HV2G HUMAN	HV60_MOUSE
DB	~	~	N	N	~	~	~	0	~	N	~	~	N	N	н	~	7	~	~	~	н	N	~	N	~	~	~	7	~	-	-
\$ Query Match Length	119	465	476	477	150	576	479	620	478	492	139	496	136	483	137	119	595	597	597	625	146	597	130	115	478	120	615	290	119	117	116
& Query Match	79.4	79.0	75.7	75.0	74.3	74.3	73.4	73.2	71.8	71.7	71.1	71.1	71.0	71.0	70.7	9.69	69.4	69.4	69.4	69.4	69.4	69.1	67.8	67.4	67.0	67.0	6.99	9.99	66.1	62.9	65.4
Score	496	493.5	473	468.5	464.5	464.5	459	457.5	448.5	448	444.5	444.5	443.5	443.5	442	435	434	434	434	434	433.5	432	423.5	421	419	418.5	418	416	413	412	409
Result No.		7	m	4	Ŋ	<b>9</b>	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31

Q723y6 homo sapien Q53vg4 mus musculu P01824 homo sapien Q6mzx7 homo sapien Q9u175 homo sapien Q51049 mus musculu Q51041 rattus norv Q6tc63 homo sapien Q51019 rattus norv Q53vg6 mus musculu Q53vg0 mus musculu Q53vg0 mus musculu Q53vg2 mus musculu Q53vg2 mus musculu Q53vg2 mus musculu Q53vg2 mus musculu Q53vg2 mus musculu Q53vg2 mus musculu
Q723Y6 HUMAN Q53VQ4 MOUSE HV2F HUMAN Q6MZX7 HUMAN Q51U,75 HUMAN Q51U,75 HUMAN Q51U,12 HUMAN Q53VR6 MOUSE Q510L9 RAT Q51U,9 RAT Q53VR2 MOUSE Q53VR2 MOUSE Q53VR2 MOUSE Q53VR2 MOUSE
10000000000000000000000000000000000000
116 98 129 129 119 477 477 473 98 98 98 98 98 98 113
64446 6446 6466 6466
403.5 403.5 402.3 397.5 398.5 398.5 398.5 398.5 398.5 398.5 398.5 398.5 398.5 398.5 398.5
W W W W W W W W W W W W W W W W W W W

# ALIGNMENTS

20 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-GYYWSWIRQPAGKGLEWIGRIYTSGSTNY 78

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TISSUE=Primary B-Cells,

NUCLEOTIDE SEQUENCE.

REDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RETAINES-2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausherg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeceberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

Rapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., McKwan P.J., McKernan K.J., Makek J.A., Gubbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Hichards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Richards S., Worley K.C., Sodergren E.J., Lu X., Gibbs R.A.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.,

Roherzation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                            60 TPSLKSRVTISVDRSKNOFSLKITSLTAADTAVYFCARLSNWGPYYFDYWGQGTLVTVSS 119
                                                                                                                                        61 KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR---YGRVFFDYWGQGTLVTVSS 117
QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY 60
                                                                    59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                           QVQLQESGPGLVKPSETLSLTCTVSGGSIC-SYYWSWIRQPPGKGLEWIGYIYYSGSTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.0%; Score 493.5; DB 2; Length 465; 83.8%; Pred. No. 2.1e-41; ive 4; Mismatches 14; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073766; AAH73766.1; -; mRNA.

R GO; GO:0016021; C:integral to membrane; IEA.
InterPro; IPR001599; Ig.
InterPro; IPR001599; Ig.
InterPro; IPR001599; Ig.
InterPro; IPR001599; Ig.
InterPro; IPR001596; Ig.
InterPro; IPR001696; IRR001696; I
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SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 2.
                                                                                                                                                                                                                                                                                                                                                                                 QGGMX6 HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                             RESULT
Q6GMX6
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MEDLINE=22380257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22380257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22380257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Fealingold B.A., Grouse L.H., Derge J.G.,

RA Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altachins R.F., Jordan H., Moore T., Max S.I., Wang J., Hate N.K.,

Brapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brapleton M., Gazes M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton B., Ketteman M., Radan A., Rodrigues S., Sanchez A.,

Rahey J., Helton B., Ketteman M., Green E.D., Dickson M.C.,

Rahesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rahesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rodriguez C.M., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human

RI M. Machan P.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79 NPSLKSRVTMSVDTSKNOFSLKLSSVTAADTAVYYCARGRFTYFDYMGOGTLVTVSS 135
                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
61 KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75.7%; Score 473; DB 2; Length 476; 74.8%; Pred. No. 2.6e-39; ive 10; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
SEQUENCE 476 AA; 52286 MW; 622AABASC62DDE9D CRC64;
                                                                                                                                                05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Home sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                26GMX1_HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rissum=Spleen;
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Local Si.
95; C
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                                                                                                    HUMAN
                                                                                                                                      Q6GMX1;
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                                                                                 RESULT 3
                                                                                                    OGGMX1
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Gaps

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1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY

98; Conservative

Best Local Similarity

Matches

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Q6GMX7

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Harindranath N., Goldfarb I.S., Ikemateu H., Burastero S.E.,
Milder R.L., Notkins A.L., Casali P.;
Milder R.L., Notkins A.L., Casali P.;
"Complete sequence of the genes encoding the VH and VL regions of low-
read high-affinity monoclonal 18M and 18A1 rheumatoid factors produced
by CD5+ B cells from a rheumatoid arthritis patient.";
Int. Immunol. 3:865-875(1991).
Int. Immunol. 3:865-875(1991).
PIR; 331673; AAC79084.1; -; mRNA.
PIR; 331673; AAC79084.1; -; mRNA.
PIR; 378056; S78056.
RISSP, PO1820; 1677.
RISSP, PO1820; 1677.
RISSP, PO1820; 1677.
RICEPPO; IPRO0710; Ig-like.
RICEPPO; IPRO07596; Ig-V.
                                                                                  KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRVF---FDYWGQGTLVTVSS 117
                                                                                                                79 NPSLKSRVTLSLDTSKNQFSLRLNSVTAADTAVXYCA-HGSSWDFAFDXWGQGTLVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
20 QVQLQESGPGLVXPSETLSLTCTVSGGSIS-SYYWSWIRQTAGKGLEWIGYISHSGSTTX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.; In the synovium of "Clonal proliferation of IgM secreting B cell in the synovium of Behcet's patient with arthritis."; Submitted (OCT-1998) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74.3%; Score 464.5; DB 2; Length 150; 77.1%; Pred. No. 5.4e-39; ive 8; Mismatches 18; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VH4 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 19 Potential.
20 >150 WH4 heavy chain variable 1
150 150 MW; 85664E04938AA7C9 CRC64;
                                                                                                                                                                                                                                                                                                                    01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAX-2004 (TrEMBLrel. 26, Last annotation update)
WH4 heavy chain variable region precursor (Fragment)
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QEP418;
                                                                                                                                                                                                                                                                     095973 HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=1718404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON TER
SEQUENCE
                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=IGM
                                                                                                                                                                                                                                            HUMAN
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TISSUE-Primary B-Cells;

XX TISSUE-Primary B-Cells;

XX TISSUE-Primary B-Cells;

XX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XI Alusner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,

XI Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Distributor, L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

XX Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

XX Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

XX Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

XX Bosak S.A., McKwan P.J., McKernan K.J., Mallek J.A., Gunarathe P.H.,

XX Hichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XX Hilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

XX Halton B., Ketreman M., Madan A., Rodrigues S., Sanchez A.,

XX Hill M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

XX Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

XX Schein J. S., Jone S.J., Warra M.A.,

XX Schein J. S., Jone S.J., Marra M.A.,

XX Schein J. S., Jone C., Sharinski M.I., Skalska U., Smailus D.E.,

XX Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
           60 YKPSLKDRVTISVDTSKNQPSLKLSSVTAADTAVYYCARYG----RVF----FDYWGQG 110
                                         80 YNPSLKSRVTISLDTSKNQFSLKANSVTAADTAVYFCARAGVWGSPRSWAIDGFNIWGQG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51631 MW; 9FE59C09C50CFF85 CRC64;
                                                                                                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypotheital protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO, GO:0016021; C:integral to membrane; IEA.
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig-like.
InterPro; IPR003597; Ig-li.
InterPro; IPR003596; Ig-li.
INTERPRO; IRR004007; IG-li.
INTERPRO; IRR004007; IG-li.
                                                                                                                                                                                                                                                                                                   477 AA.
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PROSITE; PS00290; IG MHC; UNKNOWN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; BC073765; AAH73765.1; -; mRNA.
SMR; Q6GMX7; 247-455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 78.31
Matches 94, Conservative
                                                                                                                                                                                                                                                                                        QGGMX7_HUMAN PRELIMINARY;
Q6GMX7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
SEQUENCE 477 AA; 5
                                                                                                                TLVTVSS 117
                                                                                                                                                                  140 TMVTVSS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOFIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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1 QVQLQESGPGLVKPSETLSLTCTVSGYSISG-GYLWNWIRQPPGKGLEWIGYISYDGTNN 59
                    20 QLQLQESGPGLVKPSETLSLSCTVSGGSISSTNYYWGWIRQPPEKGLEWIGSLHNSGSDY 79
                                                                       60 YKPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                  576 AA
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                                                                                                                                                                                                                                                                                             IGHD protein.
                                                                                                                                                                RESULT 6
Q6P418 F
1D Q6F
AC Q6F
DT 05-
DT 05-
DT 05-
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1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY 60

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Gaps

1;

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Name=LOC238447;
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                                                                                                                                                                             RECOURSE Primary B-Cells,

RECOURSE PRIMARY B-Cells,

RECOURSE PRIMARY B-Cells,

RECOURSE L.W., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Modin T.B., Toshiyuki S., Carninoi P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Sheychenko Y., Bouffard G.G.,

ROdriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rechnerch A., Schein J.B., Jones S.J.M., Marra M.A.,

Refeneration and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRVFF---DYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87 NPSLKSRVTISVDKSKNOFSLKLSSVTAADTAVYYCASLGDIYYYGMDVWGQGTTVTVSS 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98
                      Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 QVQLQESGPGLVKPSGTLSLTCAVSGGSISSSNWMSWVRQPPGKGLEWIGEIYHSGSTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | InterPro; | IRRO0110; | Ig-like. | InterPro; | IRR00110; | Ig-like. | InterPro; | IRR00110; | Ig-like. | InterPro; | IRR003509; | Ig-like. | InterPro; | IRR003006; | Ig-MHC. | InterPro; | IRR003506; | Ig-MHC. | InterPro; | IRR003506; | Ig-MHC. | InterPro; | IRR00407; | Ig-like. | Irror | Irr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74.3%; Score 464.5; DB 2; Length 75.8%; Pred. No. 2.3e-38; ive 7; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.; Strausberg R.; Strausberg R.; Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BC0651384; AAH63384.1; -; mRNA. HSSP; P01820; 1A7N. Ensembl; ENGG0000196122; Homo sapiens.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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01-UUN-2001 (TrEMBLrel. 17, Last seqn
01-MAR-2004 (TrEMBLrel. 26, Last ann
LOC238447 protein.
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Q99M22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 75.8 les 91; Conservative
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                                                                                                                                                                   NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE
                                                                                                                 NCBI_TaxID=9606;
  Name=IGHD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Q99M22_MC
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TESUE=MEMERAY FURING.

KR. TISSUE=MEMERAY LUGF alpha model. 7 months old;

KR. TISSUE=MEMERAY LUGF.

KR. TISSUE=MEMERAY LUGG.

KR. TISSUE=MEMERAY LUGG.

KR. TISSUE=MEMERAY LUGG.

KR. MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

KR. MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

KR. Alteschul S.F., Zeeberg B.A., Ragner L., Shemmen C.M., Schuler G.D.,

KR. Alteschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

By Lischenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brapheton M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Roberts S.M., McEwan P.D., McKernan K.J., Malk J., Fullyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A. C., Grimutz J., Myers R.M.,

Richards V., Hallon B.W., Green E.D., Dickson M.C.,

Mitching M., Madan A., Young A. C., Shevchenko Y., Bouffard G.G.,

Butterfield Y.S.N., Krzywinski M.I., Sahalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Shalska U., Smailus D.E.,

R. Monse, Chin Lial analysis of more than 15,000 full-length human
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 VQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNYK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 PSLKNRISITRDTSKNQPPLKLNSVTTEDTATYYCASRGYSWFPNWGQGTLVTVSA 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old; NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            479 AA; 51992 MW; 768E39A138918892 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                620 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0003823; R:antigen binding; IEA. InterPro; IPR007110; Ig-1ike. InterPro; IPR003597; Ig c1. InterPro; IPR003006; Ig WHC. InterPro; IPR003596; Ig V. Pfam; PF07654; C1-8et; Z. SMART; SM00406; IGV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART, SM00406, IGV; 1.
PROSITE; PS50835, IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; BC002091; AAH02091.1; -; mRNA.
HSSP; P01820; 1G7J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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01-DEC-2001 (TEMBLEAL 19,
01-MAR-2004 (TEMBLEAL 26,
IGHM protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q96EYO HUMAN PRELIMINARY;
Q96EYO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.
                                                                                               Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunoglobulin domain
                                                                                                                                                           [1] T
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Mix FVB/N;
                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUMAN
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S 138
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                      146 S 146
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Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toobhyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raba S.S., McKennan R.J., Marke J.A., Gubbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska W.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Mannan and malysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPAGKGLEWIGRIYTSGSTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neale G.A., Kitchingman G.R., "mRNA transcripts initiating within the human immunoglobulin mu heavy chain enhancer region contain a non-translatable exon and are extremely heterogeneous at the 5' end.";
Nucleic Acids Res. 19:2427-2433 (1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                   TISSUE=Primary B-Cells;
MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.2%; Score 457.5; DB 2; Length 620; 78.5%; Pred. No. 1.3e-37; ive 3; Mismatches 18; Indels 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00407; IGC1; 4.
SMART; SM00406; IGV; 1.
PROSITE; PS500835; IG_LIKE; 5.
PROSITE; PS002290; IG_MC; UNKNOWN 3.
SEQUENCE 620 AA; 68125 MW; 990A1A4A6E8FF27B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; BC011857; AAH11857.2; -; mRNA.
PIR; S15590; 815590.
HSSP, PO1820; 107J.
SMR; Q96EYO; 27-251.
Ensembl; ENSG0000130076; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig c1.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig v.
Pfam; PP07654; C1-set; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 73.2
Best Local Similarity 78.5
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00409; IG; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE
                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=1904154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 S 117
  셤
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60 YKPSLKDRVTISVDTSKNOFSLKLSSVTAADTAVYYCAR---YGRVFFDYWGQGTLVTVS 116
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 QVQLQESGPGLVKPSQTLSLTCTVSGGSIGSGDYFWSWIRQAPGRGLEWMGYIYYSGSTX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLQESGPGLVXPSETLSLTCTVSGYSI-SGGYLWNWIRQPPGKGLEWIGYISYDGTNN
                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Human rectum tumor;
Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A., Stobo G., Han M., Wiemann S.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX338066; CAD97996.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.8%; Score 448.5; DB 2; Length 478; 72.7%; Pred. No. 8e-37; Live 14; Mismatches 14; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp686C02218 (Fragment)
Name=DKFZp686C02218;
Homo sapiens (Human)
                                                       01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp686K04218 (Fragment).
Name=DKFZp686K04218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ensembl; ENSG0000130076; Homo sapiens.
Ensembl; ENSG0000130076; Homo sapiens.
InterPro; IPR00310; 19-14ke.
InterPro; IPR003597; 19_c1.
InterPro; IPR003597; 19_w.
InterPro; IPR003596; 19_w.
Pfam; PF07654; C1-set; 2.
PROSITE; PS50835; 1G_LIKE; 4.
PROSITE; PS00290; 1G_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q7z374_HUMAN PRELIMINARY;
Q7Z379 HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                         NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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1; Gaps

8; Indels

88.8%; Pred. No. 5.3e-37; Live 2; Mismatches 8

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87; Conservative
            Best Local Similarity
                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 YSPSLKSRLTIFVDTSKNHFSLRLTSVTAADTAVYYCVRHVEGPYG--\#FDP\#GGGGTLVT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QVQLQESGPGLVKPSETLSLTCTVSGYSISG-GYLWNWIRQPPGKGLEWIGYISYDGTNN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 ÓLÓLÓESGPGLVKPSETLSLTCTVSGGSVSNRNYYWGWIRQPPGKGLEWIGSIYYNENTY 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
TISSUE-Human rectum tumor;

Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
Submitted (July-2003) to the Embil/GenBank/DDBJ databases.

EMBL; BX538077; CAD98001.1; -; mRNA.
RNS; O72374; 262-470.
RNS; O72374; 262-470.
Rnsembl; ENSG0000130076; Homo sapiens.
RnterPro; IPR003106; 1g-Mrc.
RnterPro; IPR003106; 1g-W.
RnterPro; IPR003596; 1g-V.
RnterPro; IPR003596; 1g-V.
RnterPro; IPR003596; 1g-V.
RMRT; SM04406; IGW; 1.
RNSPROSITE; PS06395; IG_LIKE; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Full-length cDNA clone CSODL004YM19 of B cells (Ramos cell line) of
Homo sapiens (Human) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.1%; Score 444.5; DB 2; Length 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71.7%; Score 448; DB 2; Length 49; 74.0%; Pred. No. 9.3e-37; ive 7; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=B cells;
Li W.B., Gruber C., Jessee J., Polayes D.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genoscope;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX248300; CAD62627.1; -; mRNA.
HSSP; D1209; LG7J.
SMR; Q86SX2; 33.129.
Ensembl; ENSG00000130076; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 AA; 15573 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro, IPR007110; Ig-like.
InterPro, IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q86SX2 HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein-
NON TER 1
SEQUENCE 492 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rissum=B cells;
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0865XZ
HUM
0865XX
AC 0865X
AC 0865X
DT 01-JU
DT 01-JM
DT 01-JM
DD 01-JM
DD
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MEDLINE-221805.

TISSUE-LONG;

MEDLINE-221805.

MEDLINE-221805.

MEDLINE-221805.

A lausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A laschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A laschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A pokins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

B datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Frange C.,

B rownstein M.J., Usdul T.B., Toshiyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahesley J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                               33 QVQLQESGPGLVKDSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGYIYYSGSTNY
1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC016369; AAH16369.1; -; mRNA.
HSSP; PO1876; LDW0.
SMR; Q96KX8; Z66-474.
Ensembl; ENSG00000130076; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        496 AA; 53392 MW; D346929849040D69 CRC64;
                                                                                                                                                                                                                 92 NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                 61 KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN_1.
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003106; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP07654; C1-get; 2.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                            OJOGENSE HUMAN PRELIMINARY;

OJOGENSE HUMAN PRELIMINARY;

OJOGENSE HUMAN PRELIMINARY;

OJOGENSE HUMAN PRELIMINARY;

OJOGENSE HUMAN OJOGENSE OJOGENS
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HV46 MOUSE
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HV46_MOUSE
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                                                                                                   MEDLINE=90067954; PubMed=2587273;

A Urakov D.N., Deev S.M., Polyanovsky O.L.;

The structure of the expressible VH gene from a hybridoma producing monoclonal antibodies against porcine transferrin.";

INCleic Acids Res. 17:9481-9481(1989).

EMBL; X16740; CAA34714.1; -; Genomic_DNA.

RISSP; P18532; IKCV.

R HSSP; P18532; IKCV.

R INCLEPRO; IPR003599; IG.

R INCLEPRO; IPR003599; IG.

R INCLEPRO; IPR003596; IG.

R INCLEPRO; IPR003596; IG.

R SMART; SM00409; IG; 1.

R SMART; SM00406; IGV; 1.

R PROSITE; PS50835; IG_LIKE; 1.
                      20 QLQLQESGPGLVKSSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIANTYYSGITY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 VQLQESGPGLVKPSFTLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNYK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 VQLQESGPGLVKPSQSLSLTCSVTDFSITSGYYWHWIRQFPGNKLEWMGYISYDGSNGYN 79
OVOLOESGPGLVKPSETLSLTCTVSGYSI - SGGYLWNWIROPPGKGLEWIGYISYDGTNN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 PSLKDRVTISVDTSKNOFSLKLSSVTAADTAVYYCAR-YGRVFPDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 PSLKNRISITRDTSKNQFFLKLNSVTTEDTATYYCTRGDGYHFFTYWGQGTLVTVSA 136
                                                                                  YKPSLKDRVTISVDTSKNOFSLKLSSVTAADTAVYYCARYG-----RVFFDYWGQGTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71.0%; Score 443.5; DB 2; Length 136; 70.9%; Pred. No. 6.5e-37;
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                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83; Conservative 15; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Z
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                                                                                                                                                                                                                                                                                                                                                                                                                              (Fragment).
                                                                                                                                                                                                                                                                                                           QGLBQS_MOUSE PRELIMINARY;
Q6LBQS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QSU413_MOUSE PRELIMINARY;
QSU413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
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                                                                                                                                                                    114 TVSS 117
                                                                                                                                                                                                         140 TVSS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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Н
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C91413 MOUSE
LD C50413_M
C91413_M
C91413_M
C91 C1-FEB-2(
D7 01-FEB-2(
D7 01-FEB-2(
D8 Name-LOC(
C9 Mus muscr
C0 Entsaryote
C0 Entsaryote
C0 Musmalia,
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STRAINE-EVBN'N, TISSUE-Colon,

MEDLINE=2238827; PubMed=1247992; DOI=10.1073/pnag.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusham K., Parmer A.A., Rubin G.M., Hong L.,

Biatchenko L., Marusham K., Parmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

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Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Wetteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

An Hakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Roberstion and initial analysis of more than 15,000 full-length human
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01-AUG-1992 (Rel. 23, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
10-MAY-2005 (Rel. 47, Last annotation update)
1g heavy chain V region MOPC 315 precursor.
Mus musculus (Mouse).

Musmyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euzronoteoglires; Glires; Rodentia; Sciurognathi;
Mucoidea; Murinae; Mus.
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NUCLEOTIDE SEQUENCE.
MEDLINE=89238351; PubMed=2497341; DOI=10.1016/0161-5890(89)90133-8;
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                                                                                                                                                                                                                                                                                       MEDLINE=74170779; PubMed=4524622; Francis S.H., Leslie R.G.Q., Hood L., Eisen H.N.; Manino-acid sequence of the variable region of the heavy (alpha) chain of a mouse myeloma protein with anti-hapten activity."; Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).
Rinfret A., Horne C., Dorrington K.J., Klein M.;
"Cloning, sequencing and expression of the rearranged MOPC 315 VH gene
segment.";
                                                                                                                                                                                PROTEIN SEQUENCE OF 1-21.
MEDLINE=79148758; PubMed=428562;
Schechter I., Wolf O., Zemell R., Burstein Y.;
"Structure and function of immunoglobulin genes and precursors.";
Fed. Proc. 38:1839-1845(1979).
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE REVISION TO 53.

MEDLINE=77244979; PubMed=268248;
MODLINE=77244979; PubMed=268248;
Mod L., Margolies M.N., Givol D., Zakut R.;
Unpublished results, cited by:
Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;
Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).
-!- MISCELLANEOUS: This alpha chain was isolated from a myeloma protein that has anti-dinitrophenyl activity.
                                                                            PROTEIN SEQUENCE OF 1-31.
MEDDLINE-78094475; PubMed=414225;
Jilka R.L., Petka S.;
"Amino acid sequence of the precursor region of MOPC-315 mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chain V region MOPC 315.
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G -> GG (in Ref. 1; CAA30727).

G -> H (in Ref. 2).

GY -> YG (in Ref. 4).

N -> D (in Ref. 4).

Missing (in Ref. 4).
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                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696(1977).
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PROSITE; PSS0835; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region; Signal.
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EMBL; X07880; CAA30727.1; -; Genomic_DNA.
PIR; PLO102; AVMS35.
HSSP, PO1820; 1G7J.
SMR; PO1822; 20-137.
ENSEMD1; ENSWIGGGOOO055748; Mus musculus.
InterPro; IPR00710; IG-like.
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                                              Mol. Immunol. 26:431-434(1989).
                                                                                                                                         immunoglobulin heavy chain."
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Best Local Similarity 69.55
Matches 82; Conservative
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20 VQLQESGPGLVKPSQSLSLTCSVTGYSITSGYF#NWIRQFPGNKLEWLGFIKYDGSNGYN 79
2 VQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNYK 61
                                                                                                                                                                       62 PSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCA--RYGRVFFDYWGQGTLVTVSS 117
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completed: January 10, 2006, 20:53:28 Search comp Job time :

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January 10, 2006, 20:55:23; Search time 5.96642 Seconds (without alignments) 166.558 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USO1_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USO1_NEW_PUB.pep:*
GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES		US-11-012-353-79	US-11-012-353-81	US-11-012-353-7	US-11-012-353-7	US-11-012-353-83	US-11-012-353-85	US-11-012-353-69	US-11-012-353-52	US-11-012-353-162	US-11-012-353-7	US-11-012-353-7	US-11-054-	<b>JS-11-054-515-1548</b>	JS-11-012-353-72	US-11-102-201	US-11-054-	US-10-721-763-17	US-10-512-184-34	US-10-512-184-71	US-10-512-184-49	US-11-054-515-1994	US-11-054-515-1329	US-11-054-669-112	US-11-054-669-11	US-11-054-515-84
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# ALIGNMENTS

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Sequence 79, Application US/11012353
; Sequence 79, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: GOETSCH, NATHALIE
; APPLICANT: BAEUW, JEAA-FRANCOIS
; APPLICANT: HAEUW, JEAA-FRANCOIS
; APPLICANT: HAEUW, JEAA-FRANCOIS
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: NECEPTORS ANTIBODIES AND USES THEREOF
; FILE REPERENCE: 017753-198
; CURRENT PILIAN DATE: 2004-12-16
; PRIOR FILING DATE: 2003-01-20
; PRIOR FILING DATE: 2003-01-20
; PRIOR FILING DATE: 2003-01-20
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Pred. No. 1.2e-48;
; Mismatches 0; Indels
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CORGANISM: Homo sapiens
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PRIOR APPLICATION NUMBER: FR 0200653
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 0200654
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARE: PATENTIN VET: 3.3
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                                                                                        US-IL-012-353-81

Sequence 81, Application US/11012353

PUBLICANT 0. US20050249730A1

GENERAL INFORMATION:
APPLICANT: GORYALA, NATHALIE
APPLICANT: CORVALA, NATHALIE
APPLICANT: DIFLOS, ALAIN
APPLICANT: BECK, ALAIN
APPLICANT: USCEPTORS ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-198
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT PAPLICATION NUMBER: 10/735,916
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-07-120
PRIOR PILING DATE: 2003-01-20
PRIOR PILING DATE: 2002-01-20
PRIOR PILING DATE: 2002-01-20
PRIOR PILING DATE: 2002-01-18
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Publication No. US20050249730A1

GENERAL INFORMATION:

APPLICANT: GORYCH, LILIANE

APPLICANT: CORVAIA, NATHALIE

APPLICANT: DUFLOS, ALAIN

TITLE OF INVENTION: NOUSE ANTIBODIES AND USES THEREOF

TITLE OF INVENTION: NECEPTORS ANTIBODIES AND USES THEREOF

TITLE OF INVENTION: NUMBER: US/11/012,353

CURRENT FILING DATE: 2003-12-16

PRIOR FILING DATE: 2003-07-11

PRIOR FILING DATE: 2003-07-11

PRIOR FILING DATE: 2003-07-21

PRIOR PLILING DATE: 2003-01-20

PRIOR FILING DATE: 2003-01-20

PRIOR FILING DATE: 2003-01-20

PRIOR FILING DATE: 2003-01-20

PRIOR PLILING DATE: 2003-01-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-81
                                                                                     11-012-353-81
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Sequence 77, Application US/11012353

Publication No. US20050249730A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GOETSCH, LILIANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
TITLE OF INVENTION: ARECEPTORS ANTIBODIES AND USES THEREOF
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
TITLE OF INVENTION NUMBER: US/11/012,353
CURRENT APPLICATION NUMBER: 10/735,916
FILE REFERENCE: 2003-07-11
PRIOR FILING DATE: 2003-07-11
PRIOR PLILING DATE: 2003-07-11
PRIOR PLILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-07-11
PRIOR PLILING DATE: 2003-07-11
PRIOR PRILING DATE: 2003-07-11
PRIOR PLILING DATE: 2003-07-13
PRIOR PLILING DATE: 2003-07-13
SEQUENCE OF SEQUENCE PRIOR PLILING DATE: 2003-07-13
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                                                                                                                                                                                                                                                         1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY 60
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                                                                                        Gaps
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Query Match 99.4%; Score 623; DB 7; Length 117; Best Local Similarity 98.3%; Pred. No. 2.7e-48; Matches 115; Conservative 2; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: FR 0205753
PRIOR FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: FR 0200653
PRIOR FILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARE: Patentin Ver. 3.3
SEQ ID NO 85:
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; ORGANISM: Mus musculus
US-11-012-353-69
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CORGANISM: Homo sapiens
US-11-012-353-85
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Best Local Similarity
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                                                                                                                                        Sequence 83, Application US/11012353
Publication No. US20050249730A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
JAPPLICANT: GORYSCH, LILIANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
JAPLICANT: BECK, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
FRICK APPLICATION NUMBER: PR 0308538
PRIOR FILING DATE: 2003-12-16
PRIOR FILING DATE: 2003-01-20
PRIOR FILING DATE: 2002-05-07
PRIOR FILING DATE: 2002-05-07
PRIOR FILING DATE: 2002-01-18
PRIOR PRILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR PRILING DATE: 2002-01-18
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Publication No. US20050249730A1
GENERAL INFORMATION:
APPLICANT: GORTSCH, LILIANE
APPLICANT: GORTSCH, LILIANE
APPLICANT: DUFLOS, ALAIN
APPLICANT: HAEW, JEAN-FRANCOIS
APPLICANT: HAEW, JEAN-FRANCOIS
APPLICANT: HECER, OLIVIER
APPLICANT: HECER, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND USES THEREOF
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-198
CURRENT APPLICATION NUMBER: 10/735,916
PRIOR FILING DATE: 2003-12-16
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-07-11
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98.1%; Score 615; DB 7;
Best Local Similarity 98.3%; Pred. No. 1.4e-47;
Matches 115; Conservative 1; Mismatches 1;
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; ORGANISM: Homo sapiens
US-11-012-353-83
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US-11-012-353-69

US-11-012-353-69

Sequence 69, Application US/11012353

Publication No. US20050249730A1

GENERAL INPORMATION:

APPLICANT: GORVAIA, NATHALIE

APPLICANT: CORVAIA, NATHALIE

APPLICANT: DUELOS, ALAIN

APPLICANT: HAEUW, JEAN-FRANCOIS

APPLICANT: HEGEN, OLIVIER

APPLICANT: HEGEN, OLIVIER

TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

TITLE OF INVENTION NUMBER: 10/735,916

PRIOR PELLING DATE: 2003-12-16

PRIOR PILLING DATE: 2003-07-11

PRIOR PELLING DATE: 2003-07-11

PRIOR PILLING DATE: 2003-07-11

PRIOR PILLING DATE: 2003-07-11

PRIOR PILLING DATE: 2003-07-11

PRIOR PILLING DATE: 2002-01-08

PRIOR PILLING DATE: 2002-01-18

PRIOR PILLING DATE: 2002-01-18

PRIOR PILLING DATE: 2002-01-18

PRIOR PILLING DATE: 2002-01-18

PRIOR PILLING DATE: 2003-01-18

PRIOR PILLING DATE: 2003-01-18
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                                                                                                                                                                                                                                                                                                                                                            61 KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                     79 KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 135
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                                                                                                                                                                         1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                       Gaps
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    Length 135;
                                                                                       1; Indels
Score 615; DB 7;
Pred. No. 1.6e-47;
                                                                                  1; Mismatches
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PRIOR FILING DATE: 2003-01-20
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APPLICANT: CORNAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
APPLICANT: DUFLOS, ALAIN
APPLICANT: BECK, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
TITLE OF INVENTION: NOVELS: US/11/012,353
CURRENT APPLICATION NUMBER: 10/735,916
PRIOR PLICATION NUMBER: 10/735,916
PRIOR PELICATION NUMBER: PR 0306538
PRIOR APPLICATION NUMBER: PR 0306538
PRIOR APPLICATION NUMBER: FR 0205573
PRIOR APPLICATION NUMBER: FR 0205573
PRIOR PLIING DATE: 2002-01-18
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APPLICANT: CORVALA, NATHALIE
APPLICANT: DUFLOS, ALAIN
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: LEGER, OLIVER ANTI-INSULIN/IGF-I HYBRID
ITILE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
ITILE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
ITILE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
ITILE OF INVENTION: NUMBER: US/11/012,353
CURRENT APPLICATION NUMBER: 10/735,916
PRIOR PILING DATE: 2003-12-16
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-07-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 VQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQPPGNKLEWMGYISYDGTNNYK 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 162, Application US/11012353
Publication No. US20050249730A1
GENERAL INFORMATION:
APPLICANT: GOETSCH, LILLANE
                                                                                                                                                            Sequence 52, Application US/11012353
Publication No. US20050249730A1
GENERAL INFORMATION:
APPLICANT: GOETSCH, LILIANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-353-52
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GENERAL INVORMATION:

APPLICANT: GORVAIA, NATHALIE

APPLICANT: CORVAIA, NATHALIE

APPLICANT: CORVAIA, NATHALIE

APPLICANT: DUFLOS, ALAIN

APPLICANT: HAEUW, JEAN-FRANCOIS

APPLICANT: HEGER, OLIVIER

APPLICANT: HEGER, OLIVIER

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: NACEPORS ANTIBODIES AND USES THEREOF

FILE REFERENCE: 017733-198

CURRENT APPLICATION NUMBER: US/11/012,353

CURRENT PILING DATE: 2004-12-16

PRIOR APPLICATION NUMBER: FR 0308538

PRIOR FILING DATE: 2003-01-20

PRIOR FILING DATE: 2003-01-20

PRIOR APPLICATION NUMBER: FR 0205753

PRIOR FILING DATE: 2002-01-18

PRIOR PLILNG DATE: 2002-01-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLQESGPGLVKPSETLSLICTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 KPSLKDRVTISRDTSKNOPSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 NPSLKSRVTISVDTSKNQPSLKLSSVTAADTAVYYCARYGRVFFDYWGQCTTLTVSS 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLQESGPGLVKPSETLSLTCTVSGYSISSGYYWGWIRQPPGKGLEWIGSIFHSGSSYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 536; DB 7; Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15; Indels
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Best Local Similarity 76.1%; Pred. No. 4.8e-36;
Matches 89; Conservative 12; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . No. 1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Mismatches
PRIOR APPLICATION NUMBER: FR 0205753
PRIOR FILING DATE: 2002-05-07
PRIOR PLING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARR: PATENTIN VET. 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 70, Application US/11012353 Publication No. US20050249730A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           85.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 86.3
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patentin Ver. 3.3
                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Mus musculus
US-11-012-353-70
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61 KPSLXDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARY-----GRVF-FDYWGQGTLV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY 60
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT:

FILE REFERENCE:

CURRENT APPLICATION NUMBER:

GOS-02-10

FRIOR PALICATION NUMBER:

FRIOR PALICATION NUMBER:

FRIOR PALICATION NUMBER:

FRIOR APPLICATION NUMBER:

FRIOR FILING DATE:

FRIOR PARCE RELIGATION NUMBER:

FRIOR FILING DATE:

FRIOR PAPLICATION NUMBER:

FRIOR FILING DATE:

FRIOR FILING DA
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR PLILING DATE: 2001-12-16
PRIOR PLILING DATE: 2001-12-19
PRIOR PLILING DATE: 2001-12-19
PRIOR PLILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR PLILNG DATE: 2001-05-25
PRIOR PLILNG DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PLILNG DATE: 2001-03-16
PRIOR PLILNG DATE: 2001-03-16
PRIOR PLILNG DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR PLILNG DATE: 2001-03-16
PRIOR PLILNG DATE: 2001-03-16
PRIOR PLILNG DATE: 2001-03-16
PRIOR PLILNG DATE: 2001-10-17
NUMBER OF SEQ ID NOS: 3247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 7; Length 247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16; Indels
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Best Local Similarity 77.4%; Pred. No. 1.2e-35;
Matches 96; Conservative 5; Mismatches 16
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US-11-054-515-1548
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Publication No. US20050249730A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GORTSCH, LILIANE
APPLICANT: GORTSCH, LILIANE
APPLICANT: GORTSCH, LILIANE
APPLICANT: HACH, JEAN-FRANCOIS
APPLICANT: BECK, ALAIN
TITLE OF INVENTION: NOTEST ANTI-IGF-IR AND USES THEREOF
FILE REFERENCE: 017753-198
CURRENT APPLICATION NUMBER: 10/735,916
PRIOR FILING DATE: 2004-12-16
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-01-20
PRIOR FILING DATE: 2003-01-20
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SSOFTWARE: PATECHTIN VET: 3.3
SSOFTWARE: PATECHTIN VET: 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QVQLQESGPQLVKPSETLSLICTVSGYSISSGYYWSWIRQPPGKGLEWIGSMFHSGSSYY 60
           62 PSLKNRISITRDTSKNQFFLKLANSVTTEDTATYYCAREGYGYFPDYWGQGTTLTVSS 118
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Sequence 1651, Application US/11054515

PUBLICATION NO. US200025532A1

GENERAL IMPORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523P3

CURRENT FILING DATE: 2005-02-10

PRIOR PILING DATE: 2004-02-11

PRIOR PILING DATE: 2004-02-11

PRIOR FILING DATE: 2004-06-18

PRIOR FILING DATE: 2004-06-18

PRIOR FILING DATE: 2004-06-18

PRIOR FILING DATE: 2004-06-18

PRIOR FILING DATE: 2004-10-11
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ORGANISM: Homo sapiens
US-11-012-353-73
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LENGTH: 123
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Search completed: January 10, 2006, 21:36:24 Job time : 5.96642 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                       61 NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARVHYDILTGYLWAFDIWGQGTWV 120
                                                                                                                                                                                                                                                                                       1 QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGLEWIGSIYHSGSTYY 60
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                                                                                                                                                                                                                                         1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 72, Application US/11012353
Publication No. US20050249730A1
Publication No. US20050249730A1

APPLICANT: GORVALA, NATHALIB
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: LEGER, OLIVIER
APPLICANT: LEGER, OLIVIER
APPLICANT: LEGER, OLIVIER
APPLICANT: LEGER, OLIVIER
APPLICANT: RECK, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                             7:
                                                                                                   Length 250;
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                                                                                                                                                                          15; IndelB
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                                                                                                   Query Match 76.8%; Score 481.5; DB 7; Best Local Similarity 77.4%; Pred. No. 1.2e-35; Matches 96; Conservative 6; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
75.4%; Score 473; DB 7;
Best Local Similarity 79.5%; Pred. No. 3.2e-35;
Matches 93; Conservative 6; Mismatches 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TILE REPERRICE: 017753-198
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT FILING DATE: 2004-12-16
FRIOR APPLICATION NUMBER: 10/735,916
FRIOR APPLICATION NUMBER: 10/735,916
FRIOR FILING DATE: 2003-12-16
FRIOR FILING DATE: 2003-07-11
FRIOR FILING DATE: 2003-07-11
FRIOR FILING DATE: 2003-07-11
FRIOR FILING DATE: 2003-07-11
FRIOR FILING DATE: 2003-07-17
FRIOR FILING DATE: 2003-01-20
FRIOR FILING DATE: 2003-01-20
FRIOR FILING DATE: 2002-01-18
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COCATION: (59)
COTHER INFORMATION: Variable amino acid
US-11-012-353-72
; ORGANISM: Homo sapiens
US-11-054-515-1548
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61 KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARYG-----RVFFDYWGQGTLVTV 115
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Sequence 1, Application US/11102201

Publication No. US20050565994A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL SHELTON, David L.

APPLICANT: MANTYH, Patrick W.

ITLE OF INVENTION: METHODS FOR TREATING BONE CANCER PAIN BY
TILLE OF INVENTION: ADMINISTERING A NERVE GROWTH FACTOR ANTAGONIST
FILE REFERENCE: 51471-20021.00

CURRENT PAPLICATION NUMBER: US/11/102,201

CURRENT FILING DATE: 2004-01-019

FRIOR APPLICATION NUMBER: US 60/560,654

FRIOR APPLICATION NUMBER: US 60/560,781

PRIOR APPLICATION NUMBER: US 60/560,781

PRIOR APPLICATION NUMBER: US 60/560,781

FRIOR FILING DATE: 2004-04-07

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 120
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; OTHER INFORMATION: Synthetic Construct
US-11-102-201-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                 US-10-735-916A-79
627
1 QVQLQESGPGLVKPSETLSL......RYGRVFFDYWGQGTLVTVSS 117
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1: /cgn2_6/ptodata/1/pubpāa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd.
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US-10-735-916A-75

US-10-735-916A-83

US-10-735-916A-83

US-10-735-916A-89

US-10-735-916A-69

US-10-735-916A-69

US-10-735-916A-69

US-10-735-916A-69

US-10-383-447-24

US-10-383-447-24

US-10-383-447-28

US-10-383-447-28

US-10-389-762-128

US-10-389-762-128

US-10-309-762-128

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US-10-309-762-128

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US-10-309-762-128
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                                                                                                                                                                       1867569 seqs, 417829326 residues
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Maximum Match 100%
Listing first 45 summaries
                                       - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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98, 70, 35,	230,	114, 66, 5, A	10,0	9, 11, 142
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US-10-292-088-98 US-10-292-088-70 US-10-310-719-35	US-10-310-719-37 US-10-984-960A-20 US-10-893-576-39 US-10-805-177-2	US-10-805-177-114 US-10-292-088-66 US-10-822-306A-5 US-10-822-306A-14	US-10-309-762-10 US-10-309-762-138 US-10-706-689-10 US-10-988-360-10	US-10-822-306A-9 US-10-822-306A-11 US-10-292-088-142
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28 30	# # # # # # # # # #	333	8 4 4 4 8 0 11 5	4 4 4 6 4 3

# ALIGNMENTS

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KPSLKDRVTISRDTSKNOFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
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                                                                       SUBJECTANT: GOETSCH, Liliane
APPLICANT: GOETSCH, Liliane
APPLICANT: CORVAIA, Nathalie
APPLICANT: CORVAIA, Nathalie
APPLICANT: LEGER, Olivier
APPLICANT: LEGER, Olivier
APPLICANT: LEGER, Olivier
APPLICANT: LEGER, Alain
APPLICANT: HEEW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017733-183
CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT FILING DATE: 2003-12-16
PRIOR APPLICATION NUMBER: PR 03/08 538
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-01-20
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR PELING DATE: 2002-01-18
PRIOR FILING DATE: 2002-05-07
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PATENTIN VET: 2.1
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100.0%; Pred. No. 8.7e-48;
Artive 0; Mismatches 0;
                    Sequence 79, Application US/10735916A Publication No. US20050084906A1 GENERAL INFORMATION:
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US-10-735-916A-79
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Best Local Similarity
US-10-735-916A-79
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RESULT 2 US-10-735-916A-81 ; Sequence 81, Application US/10735916A ; Publication No. US20050084906A1

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-77
US-10-735-916A-75
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### PEDELICANT: GORTSCH, Liliane

### APPLICANT: GORTSCH, Liliane

### APPLICANT: GORTSCH, Liliane

### APPLICANT: LEGER, Olivier

### APPLICANT: LEGER, Olivier

### APPLICANT: BECK, Alain

### APPLICANT: BECK, Alain

### APPLICANT: BECK, Alain

### APPLICANT: HAEUW, Jean-Francois

### APPLICANT: HAEUW, Jean-Francois

### TITLE OF INVENTION: NOWEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF

### TITLE OF INVENTION: NOWER: US/10/735,916A

### CURRENT APPLICATION NUMBER: FR 03/08 538

### PRIOR FILING DATE: 2003-07-11

### PRIOR PILING DATE: 2003-07-20

### PRIOR FILING DATE: 2003-01-20

### PRIOR FILING DATE: 2002-01-18

#### PRIOR FILING DATE: 2002-01-18

            JOSENERAL INFUGRATION:

JAPLICANT: GORTSCH, Liliane

APPLICANT: CORVAIA, Nathalie

APPLICANT: CORVAIA, Nathalie

APPLICANT: DEGER, Olivier

APPLICANT: BECR, Alain

APPLICANT: BECK, Alain

APPLICANT: BECK, Alain

APPLICANT: HALW, Jean-Francois

TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF

FILE REFERENCE: 017753-183

CURRENT APPLICATION NUMBER: US/10/735,916A

CURRENT APPLICATION NUMBER: PR 03/08

PRIOR FILING DATE: 2003-07-11

PRIOR PILING DATE: 2003-07-12

PRIOR PILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18

PRIOR PELING DATE: 2002-05-07

NUMBER OF SEQ ID NOS: 156

SOFTWARE: PALEALIN Ver. 2.1

LEMERT OF SEQ ID NO 81
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY 60
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                                                                                                                                                                                                                                                                                                      61 KPSLKDRVTISRDTSKNOFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                            KPSLKDRITISRDTSKNOFSLKLSSVTAADTAVYYCARYGRVFFDYWGGGTLVIVSS 117
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                                                                                    Gaps
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Sequence 77, Application US/10735916A

Publication No. US20050084906A1

GENERAL INFORMATION:

APPLICANT: GORNSCH, Aliliane

APPLICANT: DUFLOS, Alain

APPLICANT: DUFLOS, Alain

APPLICANT: BECK, Alain

APPLICANT: HAEUW, Jean-Francois

TITLE REPERENCE: 017753-183

TITLE REPERENCE: 017753-183

CURRENT APPLICATION NUMBER: FR 03/08 538

FRIOR APPLICATION NUMBER: PC7/FR 03/09

FRIOR PELING DATE: 2003-01-11

FRIOR PELING DATE: 2003-01-11

FRIOR PELING DATE: 2003-01-18

FRIOR PELING DATE: 2003-01-18

FRIOR PELING DATE: 2002-01-18

FRIOR APPLICATION NUMBER: FR 02/06 654

FRIOR APPLICATION NUMBER: FR 02/05 553

FRIOR APPLICATION NUMBER: FR 02/05 573

FRIOR APPLICATION NUMBER: FR 02/05 573

FRIOR APPLICATION NUMBER: FR 02/05 573

FRIOR APPLICATION NUMBER: FR 02/05 753

FRIOR APPLICATION NUMBER: FR 02/05 753

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FRIOR APPLICATION NUMBER: FR 02/05 753
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Publication No. US20050084906A1
GENERAL INFORMATION:
APPLICANT: GORTSCH, Liliane
APPLICANT: LEGER, Olivier
APPLICANT: BECK, Alain
APPLICANT: BECK, Alain
APPLICANT: BECK, Alain
APPLICANT: HECW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Query Match 99.4%; Score 623; DB 5; Length 117; Best Local Similarity 98.3%; Pred. No. 2e-47; Matches 115; Conservative 2; Mismatches 0; Indels
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Best Local Similarity 98.31
Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 156
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 77
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2 VQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLMNWIRQFPGNKLEMMGYISYDGTNNYK 61
19 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY 78
                                                                                                                                 2 VQLQESGPGLVXPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNYK
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                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: GOETSCH, Liliane
APPLICANT: GOETSCH, Liliane
APPLICANT: GOETSCH, Liliane
APPLICANT: GOETSCH, Liliane
APPLICANT: DUFLOS, Alain
APPLICANT: DUFLOS, Alain
APPLICANT: BECK, Alain
APPLICANT: WOWEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REFERENCE: 1073-123
CURRENT APPLICATION NUMBER: R 03/09 538
FRIOR PELING DATE: 2003-01-10
PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
PRIOR PELING DATE: 2003-01-18
PRIOR APPLICATION NUMBER: FR 02/06 653
PRIOR APPLICATION NUMBER: FR 02/06 654
PRIOR APPLICATION NUMBER: FR 02/05 753
PRIOR FILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-05-07
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Publication No. US20050084906A1
GENERAL INFORMATION
APPLICANT: CORVAIA, Nathalie
APPLICANT: LEGER, Olivier
APPLICANT: BECK, Alain
APPLICANT: HAEUW, Jean-APPLICANT: HAEU
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; Sequence 69, Application US/10735916A
; Publication No. US20050084906A1
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SOFTWARE: Patentin Ver. 2.1
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USE-10-735-916A-85
USE-10-735-916A-85
USE-10-735-916A-85
USE-10-735-916A-85
USE-10-735-916A-85
USE-10-735-916A-85
USEDICALI INFORMATION:
USEDICANT: GORVAIA, Nathalie
USEDICANT: CORVAIA, Nathalie
USEDICANT: LEGER, Olivier
APPLICANT: LEGER, Olivier
APPLICANT: DUFLOS, Alain
APPLICANT: BECK, Alain
APPLICANT: BECK, Alain
APPLICANT: LEGER, Olivier
APPLICANT: BECK, Alain
APPLICANT: BECK, Alain
APPLICANT: BECK, Alain
APPLICANT: BECK, Alain
APPLICANT: DUFLOS, Alain
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APPLICANT: DUFLOS, Alain
APPLICANT: BECK, Alain
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APPLICANT: BECK, Alain
APPLICANT: BECK, Alain
APPLICANT: ON UNBER: PR 03/08 538
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-01-18
PRIOR PELING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 156
SOFTWARE PATENTIN VEY: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 98.1%; Score 615; DB 5; Length 117; Best Local Similarity 98.3%; Pred. No. 9.9e-47; Matches 115; Conservative 1; Mismatches 1; Indels
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Pred. No. 1.1e-46;
1; Mismatches 1; Indels
                                  CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT FILING DATE: 2003-12-16
PRIOR APPLICATION NUMBER: RR 03/08 538
PRIOR FILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-01-20
PRIOR PILING DATE: 2003-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR PRIOR PRIOR PRIOR PRIOR FILING DATE: 2002-07
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 83
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Best Local Similarity 98.3%;
Matches 115; Conservative 1
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ORGANISM: Homo sapiens
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LENGTH: 135
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Publication No. US20040018198A1
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APPLICANT Ramakrishnan, Vanitha
APPLICANT Ramakrishnan, Vanitha
APPLICANT Ramakrishnan, Vanitha
APPLICANT Afar, Daniel
APPLICANT: Powers, Daviel
TITLE OF INVENTION: Antibodies Against Cancer Antigen TMEFF2 and Uses Thereof
FILE REFRENCE: 0582.0138.NPUSOO
CURRENT APPLICATION NUMBER: US 60/362,837
PRIOR FILING DATE: 2002-03-07
PRIOR PRILING DATE: 2002-03-07
PRIOR FILING DATE: 2002-12-27
NUMBER OF SEQ ID NOS: 34
SEQ ID NO 26
LENGTH: 120
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Best Local Similarity 84.0%; Pred. No. 6.7e-39;
Matches 100; Conservative 6; Mismatches 10; Indels 3; Gaps
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                                                                                                                                                                                                                                                                                            Length 127;
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86.3%; Score 541; DB 5; Length 12'
Best Local Similarity 84.5%; Pred. No. 3.7e-40;
Matches 98; Conservative 10; Mismatches 8; Indels
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PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 02/00 654
PRIOR FILING DATE: 2002-01-18
PRIOR PLILING DATE: 2002-05-07
PRIOR FILING DATE: 2002-05-07
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 52
LENGTH: 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Bhaskar, Vinay
APPLICANT: de la Calle, Agustin
APPLICANT: Law, Debbie
                                                                                                                                                                                                   TYPE: PRT
CORGANISM: Mus musculus
US-10-735-916A-52
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ORGANISM: Artificial
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RESULT 10 US-10-309-762-143 ; Sequence 143, Application US/10309762

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61 KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARYGRV---FFDYWGQGTLVTVSS 117
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GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Gudas, Jean
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
FILE REFERENCE: AGGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT APPLICATION NUMBER: 60/33725
PRIOR APPLICATION NUMBER: 60/33725
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 143
LENGTH: 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95; Conservative
                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-10-309-762-143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity
Matches 95; Conserv
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                                                                                                                                                                                                                                                                                                   TYPE: PRT
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Length 120;

DB 4;

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TYPE: PRT
ORGANISM: Homo Sapiens
US-10-805-177-56
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LENGTH: 121
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APPLICANT: Bhaskar, Vinay
APPLICANT: Bhaskar, Vinay
APPLICANT: Law, Debbie
APPLICANT: Caras, Ingrid
APPLICANT: Caras, Ingrid
APPLICANT: Afar, Daniel
APPLICANT: Murray, Richard
APPLICANT: Murray, Richard
APPLICANT: Murray, Richard
APPLICANT: Murray, Richard
APPLICANT: Powers, David
APPLICANT: 2002-03-07
PRIOR PLING DATE: 2002-03-07
PRIOR FILING DATE: 2002-12-27
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.2
SEQ ID NO 28
LENGTH: 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGYIYYSGSTNY 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 NPSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCARDYGGNSYFDYWGQGTLVTVSS 118
62 PSLKDRVTISRDTSKNOFSLKLSSVTAADTAVYYCA---RYGRVFFDYWGQGTLVTVSS 117
                         62 PSLKNRISITRDTSENOFFLKLSSVTAADTAVYYCARGLRRGDYSMDYWGQGTLVTVSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCAR--YGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 504.5; DB 4
Pred, No. 5.8e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80.5%; Scc. No. 5.c. 84.0%; Pred. No. 5.c. '... 4; Mismatches 7
                                                                                                                                                          Sequence 109, Application US/10292088

Publication No. US20030211100A1

GENERAL INFORMATION:

APPLICANT: GLADUE, RONALD P.
APPLICANT: GLADUE, RONALD P.
APPLICANT: GORVALAN, JOSE

APPLICANT: JIA, XIAO-CHI

APPLICANT: JIA, XIAO-CHI

TITLE OF INVENTION: ANTIBODIES TO CD40

FILE REFERENCE: ABX-PP/3 US

CURRENT APPLICATION NUMBER: US/10/292,088

CURRENT APPLICATION NUMBER: 60/348,980

PRIOR FILING DATE: 2001-11-09

NUMBER OF SEQ ID NOS: 147

SOFTWARE: PATCHING DATE: 2011-11-09

NUMBER OF SEQ ID NOS: 147

SOFTWARE: PATCHING DATE: 2011-11-09

NUMBER OF SEQ ID NOS: 147

SOFTWARE: PATCHING DATE: 2011-11-09

NUMBER OF SEQ ID NOS: 147

SEMENT APPLICATION NUMBER: 2011-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 28, Application US/10383447; Publication No. US20040096392A1
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Best Local Similarity 84.0
Matches 100; Conservative
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CORGANISM: Homo sapiens
US-10-292-088-109
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                                                                                                                   RESULT 12
US-10-292-088-109
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APPLICANT: Landes, Gregory M.
APPLICANT: Landes, Gregory M.
APPLICANT: Landes, Binyam
APPLICANT: Chen, Francine
APPLICANT: Beazheh, Binyam
APPLICANT: Tes, Kam Fai
APPLICANT: Tes, Kam Fai
APPLICANT: Starling, Gary
APPLICANT: Starling, Gary
APPLICANT: Mezes, Peter
APPLICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 YKPSLKDRVTISRDTSKNQPSLKLSSVTAADTAVYYCARYG--RVFFDYWGQGTLVTVSS 117
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                                                                                                                                                                                                                  2 VOLOESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNYK
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APPLICANT: FOLE, Ian
APPLICANT: FOLE, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Handa, Masahisa
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: (ALX) TUMOR ANTIGEN
FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
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                                                                                                              13; Indels
Query Match 80.3%; Score 503.5; DB 4 Best Local Similarity 81.5%; Pred. No. 7.2e-37; Matches 97; Conservative 6; Mismatches 13
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Best Local Similarity 83.3%; Pred. No. 7.3e-37;
Matches 100; Conservative 4; Mismatches 13
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Publication No. US20050084449A1
GENERAL INFORMATION:
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; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 25; LENGTH: 122; TYPE: PRT: 7 TYPE: PRT: ; ORGANISM: Homo sapiens US-10-309-762-25
                                                                                                                                                                                                                                                                                          Search completed: January 10, 2006, 21:35:33
Job time : 65.1754 secs
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Scoring table:

Sequence:

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Sequence 2, A Sequence 13, Sequence 11, Sequence 11,
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APPLICANT: Pack, Peter
APPLICANT: Pack, Peter
APPLICANT: Tlag, Vic
APPLICANT: Ge, Liming
APPLICANT: Ge, Liming
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: 1251 Avenue of the Americas
CITY: New York
STREET: 1251 Avenue of the Americas
CITY: New York
STREET: 1251 Avenue of the Americas
CITY: New York
STREET: 1251 Avenue of the Americas
CITY: New York
COUNTRY: USA
ZIP: 10021
COMPUTER: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
FILING DATE: 18-FEB-1998
FILING DATE: 18-FEB-1998
FILING DATE: 18-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., ESG.
REFERENCE/DOCKET NUMBER: WORPHO/5
REFERENCE/DOCKET NUMBER: WORPHO/5
REFERENCE/DOCKET NUMBER: WORPHO/5
TELEPHONICATION INFORMATION:
TELEPHONICATION INFORMATION:
TELEPHONICATION INFORMATION:
TELEFORMANICATION INFORMATION:
TELEFORMANICATION INFORMATION:
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79.7%; Score 500; DB 2; Length 119;
Best Local Similarity 83.3%; Pred. No. 4.6e-42;
Matches 100; Conservative 4; Mismatches 12; Indels
US-09-343-698-6
US-08-325-955-6
US-08-30-820-7
US-09-273-453-7
US-09-273-453-7
US-08-36-125-5
US-08-450-578-5
US-09-017-628-5
US-09-467-903-5
US-09-467-903-5
US-09-467-903-5
US-09-467-903-5
US-09-467-903-5
US-09-467-903-5
US-09-260-527-3
US-08-450-578-11
US-08-450-578-11
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                                                                                                                                                                                                                                                                                                                                                                               Sequence 39, Application US/09025769B Patent No. 6300064
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 119 amino acide
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: protein US-09-025-769B-39
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465.5
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468.5
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    Sequence 39, Appl
Sequence 65, Appl
Sequence 65, Appl
Sequence 65, Appl
Sequence 13, Appli
Sequence 4, Appli
Sequence 64, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 25,
Sequence 25,
Sequence 25,
Sequence 77,
Sequence 11,
Sequence 11,
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Sequence 1
Sequence 1
Sequence 5
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(cgn2_6/ptodata/1/iaa/5_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6_COMB.pep:*

(cgn2_6/ptodata/1/iaa/H_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                    GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-025-769B-39

US-09-025-769B-65

US-09-490-070A-39

US-09-490-153-39

US-09-490-153-35

US-09-490-153-65

US-09-490-153-65

US-09-490-153-65

US-09-490-153-65

US-09-490-153-65

US-09-490-153-65

US-09-490-177-64

US-08-137-1170-64

US-08-137-1170-64

US-08-137-1170-69

US-09-490-070A-25

US-09-490-070A-25

US-09-490-070A-25

US-09-490-153-25

US-09-490-153-25

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US-09-138-091A-77

US-09-138-091A-77

US-09-138-091A-77

US-09-91B-148-79
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US-09-800-729-145
US-10-330-613A-5
                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                             572060 segs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                              - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
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Perfect score:
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Gaps

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                                                               61 KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFF---DYWGQGTLVTVSS 117
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9
                  1 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGYIYYSGSTNY 59
QVQLQESGPGLVXPSETL,SLTCTVSGYS1TGGYLWNW1RQPPGKGLEW1GY1SYDGTNNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York STATE: New York
                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Pack, Reter
APPLICANT: 11ag, Vic
APPLICANT: 11ag, Vic
APPLICANT: Moroney, Simon
APPLICANT: Plackthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
                                                                                                                                                                       Sequence 65, Application US/09025769B Patent No. 6300064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TELEPAX: (212)596-9000
TELEPAX: (212)596-9000
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 aminor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein US-09-025-769B-65
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US-09-490-070A-39; Sequence 39; Application US/09490070A; Patent No. 6696248

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61 KPSLKDRVTISRDTSKNOFSLKLSSVTAADTAVYYCARYGRVFF---DYWGQGTLVTVSS 117
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                                                                                                                                                                                                                           ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 119;
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Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                     Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
CORRESPONDENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79.7%; Score 500; DB 2;
83.3%; Pred. No. 4.6e-42;
cive 4; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 31,298
REFERRENCE/DOCKET UNDBER: 37629-0005
TELECOMUNICATION INPORMATION:
TELEPHONE: (202) 912-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: CURLOWN>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-490-070A-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 65, Application US/09490070A Patent No. 6696248 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (202) 912-2020
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                         CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 83.3
Matches 100; Conservative
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Query Match
Best Local Similarity 83.31
Matches 100; Conservative
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STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-490-153-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFF---DYWGQGTLVTVSS 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTEN Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
                                                                                                                     COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.7%; Score 500; DB 2; Length 119; 83.3%; Pred. No. 4.6e-42; ive 4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly) peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
STREET: 1666 K Street, N.W., Suite 300 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: EP 95 11 3021.0
PILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-490-070A-65
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; Sequence 39, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acide
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 65
                                                                                                       COMPUTER READABLE FORM:
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Best Local Similarity 83.33
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York
STATE: New York
COUNTRY: USA
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60 NPSLKSRVTISVDISKNOFSLKLSSVTAADTAVYYCARWGGDGFYAMDYWGQGTLVTVSS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGYIYYSGSTNY
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COMPUTER: IBW PC compatible
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.7%; Score 500; DB 2; Length 119; 83.3%; Pred. No. 4.6e-42; Live 4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-PEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., E8q.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPONE: (212) 596-900
TELEPAX: (212) 596-900
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH 119 amin acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jr., Esq.
Americas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECTLE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
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of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: James F.
STREET: 1251 Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10021
COMPUTER READABLE FORM:
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US-09-490-324-65
US-09-490-324-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                    60 NPSLKSRVTISVDTSKNQPSLKLSSVTAADTAVYYCARWGGDGFYAMDYWGQGTLVTVSS 119
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                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                             4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly) peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk COMPATIEN FC COMPATIEN EN PC COMPATIEN SYSTEM: PC-DOS/MS-DOS OOFBATING SYSTEM: PC-DOS/MS-DOS SOOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                   Length 119
                                                                                                                                                                                                                                                                                         12; Indels
                                                                                                                                                                                                                                              Score 500; DB 2;
Pred. No. 4.6e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-3an-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
                TELEPHONE: (212)596-9000
TELEFAX: (212)596-9000
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acids
    TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 39, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                              79.7%;
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                                                                                                                                                                                                                                                                                       Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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US-09-490-324-39
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61 KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFF---DYWGQGTLVTVSS 117
                                                                                                                                                                                                                                       60 NPSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCARWGGDGFYAMDYWGQGTLVTVSS 119
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                                                                                                                                          59
                                                                                                                         1 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGYIYYSGSTNY
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                                                                                              1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ge, Liming
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly) peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1213 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
    Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 500; DB 2;
Pred. No. 4.6e-42;
4; Mismatches 12
  Score 500; DB 2;
Pred. No. 4.6e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-F2B-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
                                                4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/S TELECOMMUNICATION INFORMATION:
TELEFHONE: (212) 596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TOPOLOGY: linear
1 MOLECULE TYPE: protein
2 SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-490-324-65
                                                                                                                                                                                                                                                                                                                                                       Sequence 65, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: (212)596-9000
(212)596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
  79.78;
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Best Local Similarity 83.3%;
Matches 100; Conservative
                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New York COUNTRY: USA
Query Match
Best Local Similarity
Matches 100; Conserv
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61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGD-GFDYWGQGTLVTVSS 117

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60 YKPSLKDRVTISRDTSKNOFSLKLSSVTAADTAVYYCAR-----YGRVFFDYWGQG 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLQESGPGLVKPSETLSLTCTVSGYSIT-GGYLWNWIRQPPGKGLEWIGYISYDGTNN
                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Tang, Trom
APPLICANT: You, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Au-Young, Janice
APPLICANT: Baughn, Mariah R.
TILLEOR INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: 15M COMPATILLE
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION DATA:
APPLICATION NUMBER:
FILING APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRENEY/AGENT INFORMATION:
REGISTRENEY/BOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                           Sequence 4, Application US/09049672A Patent No. 6135941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 473 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 78.73
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 650-855-059
TELEFAX: 650-845-4166
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PANCTUT01
CLONE: 1513264
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60 NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARWGGDGFYAMDYWGQGTLVTVSS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QVOLORSGPGLVXPSETLSITCTVSGYSI-TGGYLMYWIRQPPGKGLEWIGYISYDGTNN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGLEWIGSIYHSGSTYY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
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77.7%; Score 487; DB 2; Length 117;
Best Local Similarity 83.1%; Pred. No. 8.6e-41;
Matches 98; Conservative 4; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 497; DB 2; Length 117;
Pred. No. 8.8e-42;
3; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13 Application US/10330613A
Fatent No. 6924360
GENERAL INFORMATION:
APPLICANT Gudas, Jean
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
FILE REFERENCE: ABGENIX.022A
CURRENT APPLICATION NUMBER: US/10/330,613A
CURRENT FILING DATE: 2002-12-26
PRIOR PILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENTH: 117
                                                                                                                                                                                                                          APPLICANT: Williams, Andrew J
APPLICANT: Tempest, Philip R
APPLICANT: Holtet, Thor L
APPLICANT: Holtet, Thor L
APPLICANT: Holtet, Thor L
APPLICANT: Main, Sarah H
APPLICANT: Dackson, Helen
APPLICANT: Daramola, Olalekan
APPLICANT: Daramola, Olalekan
APPLICANTION: Improvements relating to antibodies
FILE REPERENCE: AHB/CP5775333
CURRENT APPLICATION NUMBER: US/09/720,493
CURRENT APPLICANTON NUMBER: GB 9814383.7
PRIOR PILING DATE: 1998-07-02
                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Cambridge Antibody Technology Limited
                                                                                                                                       Sequence 2, Application US/09720493
Patent No. 6827925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 82.9%;
Matches 97; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 117
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
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                                                                                        RESULT 9
US-09-720-493-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 486; DB 1; Length 123;
Pred. No. 1.1e-40;
                                    16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Mismatches
              Sequence 64, Application US/08137117D Patent No. 5795965
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               TELEX: 904136
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          77.5%;
                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 123 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                        (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 77.3
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein US-08-137-117D-64
                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
RESULT 12
US-08-137-117D-64
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US-08-436-717-64
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Sequence 64, Application US/08436717 Patent No. 5817790 GENERAL INFORMATION: APPLICANT: TSUCHIYA, Masayuki

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61 KPSLKDRVTISRDTSKNOFSLKLSSVTAADTAVYYCAR--YGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
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APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: JONES, Steven
APPLICANT: JONES, STEVEN
TITLE OF INVENTION: RESHARED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                            CUUNTER: D.C.

COUNTER: D.C.

COUNTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/436,717

FILING DATE: 24-APR.1993

APPLICATION NUMBER: WO PCT/JP92/00544

FILING DATE: 24-APR.1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/JP92/00544

FILING DATE: 24-APR.1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 4-32084

FILING DATE: 19-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 3-95476

FILING DATE: 25-APR-1991

ATCOMENTATION NUMBER: 25,258

REGISTRATION NUMBER: 25,258

RELEPRAKE (202) 672-5399

THELEPRAKE (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Mismatches
                                                                                                                                                                                 ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 69, Application US/08137117D
Patent NO. 5795965
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, JOSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 904136
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acids
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Best Local Similarity 77.34
Matches 92, Conservative
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MOLECULE TYPE: protein
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US-08-137-117D-69
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Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 NPSLKSRVTMLRDTSKNOFSLRLSSVTAADTAVYYCARSLARTTAMDYWGQGSLVTVSS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCAR--YGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
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Sequence 69, Application US/08436717
Sequence 100. 5817790
GENERAL INFORMATION:
APPLICANT: STUCHIYA, Masayuki
APPLICANT: STUCHIYA, Masayuki
APPLICANT: BENDIG, Mary
APPLICANT: SALDARHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INFERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
STREET: 3000 K Street, N.W., Suite 500
                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSER: Polley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STREET: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: READABLE FORM:
MEDIUM TYPE: PetentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIPTCATION DATA:
APPLICATION NUMBER: UP 4-32084
FILING DATE: 24-APR-192
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 19-FEB-192
FILING DATE: 25-ARR-1991
FILING DATE: 25-ARR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNEY, HAROLD C.
FILING DATE: 25-ARR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNEY, HAROLD C.
FELENCYMMUNICATION NUMBER: 25.258
REFERENCE/DOCKET NUMBER: 25.258
TELLEFAX: 904136
INFORMATION POR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
INFORMATION POR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
INFORMATION POR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
RESHAPED HUMAN ANTIBODY TO HUMAN INTERLEUKIN-6 RECEPTOR: 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 138 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-08-137-117D-69
TITLE OF INVENTION: RE. TITLE OF INVENTION: INVUMBER OF SEQUENCES: 1: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-436-717-69
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요 Š 셤

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20 QVQLQESGPGLVRPSQTLSLTCTVSGYSITSDHAMSWVRQPPGRGLEWIGYISYSGITTY 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.5%; Score 486; DB 1; Length 138; 77.3%; Pred. No. 1.3e-40; ive 9; Mismatches 16; Indels
COUNTRY 10.5

ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
FILING DATE: 24-APR-1993
APPLICATION NUMBER: US/08/137,117
FILING DATE: 24-APR-1992
FILING DATE: 24-APR-1992
FILING DATE: 19-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/416
FILING DATE: 19-ERB-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/4
FILING DATE: 19-ERB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JS-25-88
REGISTRATION NUMBER: 25,258
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 25,258
REFERENCE/OFCET NUMBER: 25,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: January 10, 2006, 20:58:05 Job time : 23.847 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 904136
INFORMATION FOR SEQ ID NO: 6SEQUENCE CHARACTERISTICS: LENGTH: 138 amino acids TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 77.33
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-436-717-69
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5.1.6
Compugen Ltd.
GenCore version Copyright (c) 1993 - 2006
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OM protein - protein search, using sw model

January 10, 2006, 20:28:02; Search time 14.1157 Seconds (without alignments) 797.508 Million cell updates/sec Run on:

US-10-735-916A-79 627 Title: Perfect score:

1 QVQLQESGPGLVKPSETLSL......RYGRVFFDYWGQGTLVTVSS 117 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES	
Result	3000	Query	Query	9	£	Description
NO.	acore	March .	rengru	9 ;	at a	Description
н	509	81.2	140	~	137782	variab
8	494		130	7	831690	heavy cha
m	481	76.7	123	~	S30530	heavy chain
4	478		147	7	813519	heavy chain
'n	469.5	74.9	118	~	S24443	heavy
9	468	74.6	155	~	831511	Ig heavy chain - h
7	463.5	73.9	130	~	S30534	heavy
œ	463.5	73.9	139	~	S31586	Ig heavy chain V r
σ	462.5	73.8	129	~	S44114	heavy
10	462	73.7	155	7	\$31512	heavy
11	461.5	73.6	140	N	S78052	heavy
12	459.5	73.3	145	~	S78055	heavy
13	458	73.0	121	~	837200	heavy
14	457	72.9	121	~	844113	heavy
15	456	72.7	140	7	A49045	g heavy
16	455.5	72.6	136	~	807637	g heavy
17	455	72.6		N	S78051	g heavy chain
18	454	72.4		н	AVMS35	heavy
19	453.5	72.3		7	S38718	heavy
20	452.5	72.2	137	~	S31676	Ig heavy chain V r
21	452	72.1		~	S09711	heavy chain
22	450.5	71.9	126	~	S47010	heavy chain
23	450	71.8	117	~	I28195	g heavy chain
24	447.5		118	~	S20780	heavy chain
25	447	71.	119	~	E25114	Ig heavy chain V r
56	446		140	~	A24770	ypothetical hy
27	439.5	70.1	118	~	A26340	g heavy
28	439		119	~	C53285	chain
53	439	70.0	146	7	809710	Ig heavy chain V r

Iq heavy chain V r	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain pre	heavy	heavy chain	lambda chai	heavy chain	Ig heavy chain V r	heavy chair						
S12421	S54906	831696	S30752	B24672	826906	844125	PL0100	S30529	B26340	S26902	S19668	A41287	S12416	A25114	F25114
2	0	0	7	~	0	7	~	0	~	~	~	7	~	7	~
98	134	139	149	134	97	105	135	123	116	86	127	139	97	120	115
6.69	6.69	6.69	6.69	9.69	69.3	69.3	69.3	69.2	69.1	69.1	69.1	0.69	68.8	68.7	9.89
438	438	438	438	436.5	434.5	434.5	434.5	434	433.5	433	433	432.5	431.5	430.5	430
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

RESULT 1

	137782
_	Ig variable region (VDJ) (clone T23-9) - human (fragment)
	C;Species: Homo sapiens (man)
_	C;Date: 16-Feb-1996 #sequence revision 13-Mar-1997 #text_change 23-Jul-1999
	C; Accession: 137782; S25476
_	R;Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.
_	Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
_	A.Title: Somatic diversification in the heavy chain variable region genes expressed by
	A; Reference number: A36876; MUID:94119917; PMID:8290556
	A;Accession: 137782
	A;Status: preliminary
	A; Molecule type: mRNA
	A.Residues: 1-140 <res></res>
	A.Cross-references: UNIPARC:UPI0000176E83; EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PII
	C; Superfamily: immunoglobulin V region; immunoglobulin homology
	F;46-128/Domain: immunoglobulin homology <imm></imm>

Gaps .. 8 Query Match
81.2%; Score 509; DB 2; Length 140;
Best Local Similarity 82.9%; Pred. No. 1.9e-39;
Matches 102; Conservative 4; Mismatches 9; Indels

3, 61 KPSLKDRVTISRDTSKNOFSLKLSSVTAADTAVYYCAR----YGRVFFDYWGQGTLVT 114 9 78 20 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGYIXYSGSTNY QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY ò 셤 Š

138 VSS 140 115 VSS 117 ò 셤

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RESULT 2 S31690

C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999
B; Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A; Description: Mechanisms that generate human immunoglobulin diversity operate from the A; Accession: 331690
A; Astatus: preliminary

A,Molecule type: mRNA A,Residues: 1-130 «CUI» A,FORSE-references: UNIPARC:UP10000116471; EMBL:Z14199; NID:g30984; PIDN:CAA78568.1; PIL C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin

Gaps

. 9

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A;Cross-references: UNIPARC:UP10000115FE9; EMBD:X61650; NID:g37720; PIDN:CAA43831.1; PID R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph A;Reference number: S19663; MUID:92085276; PMID:1748994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo saplens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S31511
R;Chastsagner, P.; Demaison, C.; Theze, J.; Zouali, M.
Submitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA autc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AjStatus: preliminary
AjAndscule type: mRNA
AjRosiques: 1-155 «CHA»
AjCross-references: UNIPARC:UPI00001160FF; EMBL:X69866; NID:g33094; PIDN:CAA49500.1; PIC
CiSuperfamily: immunoglobulin V region; immunoglobulin homology
CjKeywords: heterotetramer; immunoglobulin
Fj47-129/pomain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                           60 YKPSLKDRVTISRDTSKNOPSLKLSSVTAADTAVYYCAR----YGRVPFDYWGQGTLVTV 115
                                                                                                                                                                                                                                                                                                                                    87 YNPSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCARPLLWFGEL-FDYWGGGTLVTV 145
                                                                                                                                                                                          27 QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGSIYYSGSTY 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCAR--YGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig heavy chain V region (VH4DJ) - human
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C;Accession: $24443; $19667
R;Jones, P.T.
submitted to the EMBL Data Library, October 1991
                                                                                                                                                 1 QVQLQESGPGLVKPSETLSLTCTVSGYSI-TGGYLWNWIRQPPGKGLEWIGYISYDGTNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLQESGPGLVKPSETLSLVCTVSGGSLSFSY-WGWIRQPPGKGLEWIGYISHRGSTDY
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       Length 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPARC:UP10000176B52; EMBL:X616S0
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;IS-97/Domain: immunoglobulin homology <IMM>
Score 478; DB 2;
Pred. No. 1.4e-36;
5; Mismatches 14;
Query Match 76.2%;
Best Local Similarity 79.5%;
Matches 97; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-55,57-118 < MAR>
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Matches 94; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S24443
A; Molecule type: mRNA
A; Residues: 1-118 <JON>
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                                                                                                                                                                                                                                                                                                                                                                                                                                         116 SS 117
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;Superfamily: immunoglobulin namologobulin homology
;41-125/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Side of the second of the seco
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                                                                                                                                                                                                                                                                                                                                                                                                        61 NPSLKSRVTISVDTSKNOPSLOLERSVTAADTAVYYCAR-GRYCSSTSCNWFDPWGGGTLV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVQLQESGPGLVKPSETLSLTCTVSGYSISSGYYWGWIRQPPGKGLEWIGSMFHSGSSYY 60
                                                                                                                                                                                                                                                                                           64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Species: Homo sapiens (man)
Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
Accession: S30530
                                                                                                                                                                                                                                                                         QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWSRQPPGKGLEWIGYIYYSGSTNY
                                                                                                                                                                                                                 1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KPSLKDRVTISRDTSKNOFSLKLSSVTAADTAVYYCARYGRV-----FFDYWGQGTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8;
                                                                                                                                                     10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Species: Homo sapiens (man)
C; Date: 03-Mar-1994 # Heequence_revision 10-Nov-1995 #text_change 16-2
C; Dates: 03-Mar-1994 # Heequence_revision 10-Nov-1995 #text_change 16-2
C; Accession: S30530
A; Reference number: S30520
A; Reference number: S30530
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-123 < AMAR>
A; Residues: 1-123 < AMAR>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heteroterramer; immunoglobulin
F; 15-98 / Domain: immunoglobulin homology < IWM>
                                                                      Length 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.7%; Score 481; DB 2; Length 123; ilarity 77.4%; Pred. No. 6e-37; Conservative 7; Mismatches 13; Indels
                                                                                                                                             11; Indels
                                                                          Score 494; DB 2;
Pred. No. 4.1e-38;
6; Mismatches 11
       F;20-102/Domain: immunoglobulin homology <IMM>
                                                                          Query Match 78.8%;
Best Local Similarity 78.6%;
Matches 99; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
S30530
Ig heavy chain V region - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVTVSS 130
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Best Local S:
Matches 96
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C'Accession: S44114

R'Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A; Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: UNIPARC:UPI0000116639; EMBL:231579; NID:g472968; PIDN:CAA83451.1; PI C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S31512
R;Chastespaner, P: Demaison, C:; Theze, J:; Zouali, M.
submitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto
A;Reference number: S31509
A;Accession: S31512
A;Accession: S31512
A;Accession: R31512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPARC:UPI00001160F9; EMBL:X69860; NID:g33082; PIDN:CAA49494.1; PIDC;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;47-129/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                  61 KPSLKDRVTISRDTSKNOFSLKLSSVTAADTAVYYCARYGRVF-----FDYWGQGTLV 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Speciés: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
                                                                                                                                                                                                                                                                     61 KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARYG----RVFFDYWGQGTLVTVS
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                                                                                                                                                                   20 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPAGKGLEWIGRIYTSGSTNY
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                                                                                                                  1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
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Pred. No. 3e-35;
7; Mismatches 19;
Pred. No. 2.7e-35; 5; Mismatches 16
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Best Local Similarity 73.4%;
Matches 91; Conservative
    78.5%;
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                                            95; Conservative
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-129 <HAW>
        Best Local Similarity
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submitted to the EMBL Data Library, June 1992
submitted to the EMBL Data Library, June 1992
submitted to the EMBL Data Library, June 1992
A; Description: Mechanisms that generate human immunoglobulin diversity operate from the A; Reference number: S31585
A; Reference number: S31586
A; Return: preliminary
A; Molecule type: mRNA
A; Redicule type: mRNA
A; Redicule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sycosy 19,000 applies (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens
C;Accession: S30534
A;Reference number: S30520
A;Accession: S30534
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-130 cMAR>
A;Residues: 1-130 cMAR>
A;Cross-references: UNIPARC;UPI0000113P45; EMBL;Z18320
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                               KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARYGRV--FFDY----WGQGTLV 113
                                                                                                                                                                                                                                                                                                                                                                                                        92 NPPLKSRVTISVDTSKNOFSLKVSSVTAADTAVYYCARGGGISSWYDYYGMDVWGQGTTV 151
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31586
                                                                                                                                                                                                                                                     33 QVQLQESGFGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPFGKGLEWIGYIXYTGSATY
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Pred. No. 2.5e-35;
5; Mismatches 17;
                                            74.6%; Score 468; DB 2; 76.6%; Pred. No. 1.2e-35; ive 7; Mismatches 14;
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Best Local Similarity 73.1%;
Matches 95; Conservative
                                                                                         Local Similarity 76.6
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GOGTMVTVSS 130
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73.9%; Score 463.5;

Query Match

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R; Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
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hes 93; Conserv
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A, Molecule type: mRNA
A, Residues: 1-121 <FIS>
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                                                                                                                                                                                                                                                                                                                                                                    Sydox chain precursor V-D-J region (clone mAB 63VH) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C;Accession: S78052; S23717
R;Harindranath, N.
Submitted to the EYBL Data Library, August 1990
A;Reference number: S78051
A;Accession: S78052
A;Aolecule type: mRNA
A;Residues: 1-140 cHAR>
A;Residues: S23716; MUD:92031262; PMID:1718404
A;Accession: S23717
A;Molecule type: mRNA
A;Residues: 15-111 cHAM>
A;Residues: 15-111 fergment (fragment) #status predicted cS1G>
F;15-14()Penain: signal sequence (fragment) #status predicted cANT>
F;29-111/Domain: immunoglobulin homology cIMM>
F;29-111/Domain: immunoglobulin homology cIMM>
F;29-111/Domain: immunoglobulin homology cIMM>
F;29-111/Domain: immunoglobulin homology cIMM>
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C;Species: Homo sapiens (man)
C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C;Accession: 878055, 823720
R;Harindranath, N.
Submitted to the EMBL Data Library, August 1990
A;Reference number: 878051
A;Accession: 878055
A;Accession: 679055
A;Accession: 1-145 <-HAR>
A;Residues: 1-145 <-HAR>
A;Cross-references: UNIPARC:UPIO000115E8C; EMBL:X54445; NID:g37817; PIDN:CAA38312.1; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7
  ä
                                                                                                                                   KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVF-----FDYWGQGTLV 113
                                                                                                                                                            61 KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVF------FDYWGQG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 NPSLKSRVTISVDTSKNQPSLKLSSVTAADTAVYYCARGGSVLRFLEWLLYPAFDYWGGG 133
                                             9
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                                                                                       16
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                                                                    QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGYIYYTGSATY
                                             QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
8; Gaps
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  17; Indels
  6; Mismatches
  93; Conservative
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Best Local Similarity
Matches 93; Conserv
                                                                                                                                                                                                                                                                      TVSS 155
                                                                                                                                                                                                                          TVSS 117
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Int. Immunol. 3, 865-875, 1991
A; Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
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C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Accession: 84413
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 KPSLKDRVTISRDTSKNOFSLKLSSVTAADTAVYYCAR------YGR-VFFDYWGQ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSLKDRVTISRDISKNOFSLKLSSVTAADIAVYYCARYGRV----FFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Musu-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
C;Accession: S37200
R;Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F. submitted to the EMBL Data Library, August 1993
A;Pescription: Production and cloning of TMV-specific monoclonal antibodies.
A;Reference number: S37200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 QVQLQESGPGLVKPSGTLSLTCAVSGGSISSSNWWSWVRQPPGKGLEWIGEIYHSGSTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
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                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 18-115 < HAM>
A; Residues: 18-115 < HAM>
A; Cross-references: UNIPARC:UPI00001769D2; EMBL:X54445
A; Note: the authors translated the codon GCA for residue 67 as Arg C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Reywords: immunoglobulin
F;1-17/Domain: signal sequence (fragment) #status predicted <SIG>F;18-145/Product: Ig heavy chain (fragment) #status predicted <MAT>F;32-115/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 121;
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                                                                     patient.
A;Reference number: S23716; MUID:92031262; PMID:1718404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 459.5; DB 2;
Pred. No. 6.5e-35;
6; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     th 73.0%; Score 458; DB 2; I Similarity 71.7%; Pred. No. 7.3e-35; 86; Conservative 13; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73.3%; S
milarity 72.7%; P
Conservative 6;
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Reference number: S44105

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Usery Lucesy Lines applies (mail)
C; Species: Homo sapiens (mail)
C; Species: Homo sapiens (mail)
C; Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C; Accession: A49045
Eur. J. Immunol. 22, 1781-1788, 1992
A; Title: An anti: B cell autoantibody from Wiskott-Aldrich syndrome which recognizes i blancession: A49045
A; Reference number: A49045
A; Reference number: A49045
A; Reference preliminary
A; Molecule type: DNA
A; Residues: 1-140 GRI>
A; Residues: 1-140 GRI>
A; Residues: UNIPARC: UPIO000113EDD; GB: S39381; NID: 9250899; PIDN: AAB22441.1; PID: C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Reywords: heterotetramer; immunoglobulin
F; 34-116/Domain: immunoglobulin homology < IMM>
A;Accession: S44113
A;Status: preliminary
A;Status: Draininary
A;Robecule type: DNA
A;Residues: 1-121 «HAN»
A;Residues: 1-121 «HAN»
A;Cross-references: UNIPARC:UPI000011662F; EMBL:Z31389; NID:g472967; PIDN:CAA83264.1; PI
C;Superfamaily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 YKPSLKDRVTISRDTSKNQPSLKLSSVTAADTAVYYCARYGRVF---FDYWGQGTLVTVS 116
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                                                                                                                                                                                                                                                                                                                                                          1 QVQLQESGPGLVKPSETLSLTCTVS-GYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) heavy chain V region (anti-B cell autoantibody) - human (fragment) Species: Homo sapiens (man) bate: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                    4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Gaps
                                                                                                                                                                                                                                            Ouery Match 72.9%; Score 457; DB 2; Length 121; Best Local Similarity 75.2%; Pred. No. 9e-35; Matches 91; Conservative 5; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 72.7%; Score 456; DB 2; Length 140; Best Local Similarity 75.4%; Pred. No. 1.3e-34; Matches 92; Conservative 7; Mismatches 17; Indels
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Job time : 14.1157 secs
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BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

US-10-735-916A-79

Perfect score:

Run on:

Sequence:

seq length: 0 seq length: 200000000

Minimum DB Maximum DB

UniProt\_05.80:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Database :

Query Match Length DB

Result

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mus musculu
homo sapien
rattus norv
mus musculu
rattus norv
mus musculu
                                                                                                                                      homo sapien
homo sapien
homo sapien
mus musculu
homo sapien
                    шив шивсиlи
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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PubMed=1660528;
Manheimer-Lory A., Katz J.B., Pillinger M., Ghossein C., Smith A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
PubMed=2511001;
Sanz I., Kelly P., Williams C., Scholl S., Tucker P., Capra J.D.;
"The smaller human VH gene families display remarkably little
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Myosin-reactive autoantibodies in rheumatic carditis and normal
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Q5i0j1
Q53vq9
Q53vr6
Q5i0l9
Q5i0l9
Q53vr2
Q53vg0
Q0173y6
Q9ul75
Q0123y6
Q023y6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diamond B.;
"Molecular characteristics of antibodies bearing an anti-DNA-
associated idiotype.";
J. Exp. Med. 174:1639-1652(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                            01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13219 MW; 1BDB86B6420EA0BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998)
                                                                                                                                                                                                                                                                                                                                                                         119 AA
051031_RAT
0530V6 MOUSE
HV2G HÜMAN
051019 RAT
0530V2 MOUSE
05M839_RAT
0530V2 MOUSE
HV2F HÜMAN
09UL75_HUMAN
0733V6 HUMAN
1747 MÖUSE
06MZX7_HUMAN
                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                              Q6MZX7_HUMAN
Q8TC63_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polymorphism.";
EMBO J. 8:3741-3748 (1989).
EMBL, AR015041, AAD56277.1; -; mRNA.
PIR, PH0876; PH0876.
PIR, S12416; S12416.
HSSP, PO1820; 1G7J.
SMR, Q9UL73; 1-119.
INTEATPO: IPR001710; IG-like.
INTEATPO: IPR001710; IG-like.
INTEATPO: IPR001596; IG_V.
SMART; SMO0406; IGV; 1.
NON TER 119 119
SEQUENCE 119 AA; 13219 MW; 1BDB86B
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                                                                                                                                                                                                                                                                                                                                                                       QOULTS HUMAN PRELIMINARY;
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Best Local Similarity 80.0
Matches 96; Conservative
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                                                                                                                                                                                                                                1 QVQLQESGPGLVKPSETLSL.....RYGRVFFDYWGQGTLVTVSS 117
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099m20
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                    GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                       2166443 seqs, 705528306 residues
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0723 79 HUMAN
0865X2 HUMAN
096KX8 HUMAN
053 VQ1 MOUSE
053 VQ1 MOUSE
056 986 RAT
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056998 RAT
HV2I HUMAN
053VR3 MOUSE
08WUX4 HUMAN
09BUIO HUMAN
06GWX5 HUMAN
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09BQBB HUMAN
HV60 MÕUSE
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Q81ZD7 HUMAN
Q6NYH3 HUMAN
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Q6GMX6_HUMAN
Q99M22 MOUSE
Q6GMX1_HUMAN
Q6GMX7_HUMAN
Q6LBQ5_MOUSE
Q5U413_MOUSE
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Q6P418 HUMAN
HV46 MÕUSE
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Maximum Match 100%
Listing first 45 summaries
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20 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-GYYWSWIRQPAGKGLEWIGRIYTSGSTNY 78
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WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Altsuberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A staptenon S.F., Jordan H., Moore T., Max S.I., Wang J., Hsich F.,

Diatchenco L., Marusina K.P., Farmer A.A., Rubin G.M., Hong L.,

A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Rownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

R Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

R Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

B akesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

R Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

B Rutterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,

B Robersation and initial analysis of more than 15,000 full-length human and manage of the stape of the sta
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                           1 QVQLQESGPGLVKPSETLSLTCTVSGGSIC-SYYWSWIRQPPGKGLEWIGYIYYSGSTNY
 QVQLQESGPGLVKPSETLSLTCTVSGYS1TGGYLWNWIRQPPGKGLEWIGY1SYDGTNNY
                                                                          61 KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCAR---YGRVFFDYWGQGTLVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 77.1%; Score 483.5; DB 2; Length Best Local Similarity 82.1%; Pred. No. 1.2e-41; Matches 96; Conservative 5; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.; Strausberg R.; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases. EMBL; BC07766; AAH73766.1; -; mRNA. GO; GO:0016021; C:integral to membrane; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;
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                                                                                                                                                                                                            465 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003599; IG.
InterPro; IPR007110; IG-like.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003006; Ig.MHC.
InterPro; IPR003596; Ig.v.
Pfam; PF07654; Cl-set; 3.
                                                                                                                                                                                                      QGGMK6 HUMAN PRELIMINARY;
QGGMK6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.
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SMART; SM00407; IGc1; 3.
SMART; SM00406; IGv; 1.
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1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY

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MEDLINE-2388257; PubMed-12477932; DOI=10.1073/pnas.242603899; Straubberg R.D., Peingold E.A., Grouse L.H., Derge J.G., Manuer R.D., Collins F.S., Wagner L., Derge J.G., Rausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Bronslein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Bronslein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Braha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Rohards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.G., Grimwood J., Schwchenko Y., Bouffard G.G., Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; and mouse cDNA sequences.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VOLOESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIROPPGKGLEWIGYISYDGTNNYK 61
61 KPSLKDRVTISRDISKNOFSLKLSSVTAADTAVYYCARYGRVFPDYWGQGTLVTVSS 117
                                                                79 NPSLKSRVTMSVDTSKNOFSLKLSSVTAADTAVYYCARGRFTYFDYWGQGTLVTVSS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
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TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
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EMBL; BC002091; AAH02091.1; -; mRNA.
HSSP; P01820; 1G7J.
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SEQUENCE 479 AA; 51992 MW; 768E39A138918892 CRC64;
                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                             479 AA.
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InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig-c1.
InterPro; IPR00306; Ig-MC.
InterPro; IPR003596; Ig-MC.
Pfam; PF07654; CI-8et; Z.
SMART; SM04406; IGV; 1.
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PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                             Q99M22_MOUSE PRELIMINARY;
Q99M22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                      LOC238447 protein.
Name=LOC238447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Mix FVB/N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local Similarity 77.59
Matches 93; Conservative
                                                                                                                                                                                                                                             QGGMX7 HUMAN PRELIMINARY;
QGGMX7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
TISSUE=Primary B-Cells;
                                                                           111 TLVTVSS 117
                                                                                                                         140 TMVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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HUMAN
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Attaubnerg R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopking R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Aspleton M., Soars M.B., Bonaldo M.E., Carninci P., Frange C.,

Brownstein M.J., Usdin T.B., Tonchiyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., McEwan P.J., McKernan R.J., Mazke J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glbbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Broherch A., Schein J.E., Jones S.J.M., Marra M.A.;

"" Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGDYYWSWIRQPPGKGLEWIGYIYYSGSTY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGG-YLWNWIRQPPGKGLEWIGYISYDGTNN 59
                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                              13; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 74.5%; Score 467; DB 2; Length 476; I Similarity 74.0%; Pred. No. 6.3e-40; 94; Conservative 10; Mismatches 13; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073773; AAH73773.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEQUENCE 476 AA; 52286 MW; 622AABASC62DDE9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                    476 AA
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GO; GO:0016021; C:integral to membrane; IEA.
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InterPro; IPR00110; IG-11ke.
InterPro; IPR00110; IG-11ke.
InterPro; IPR00359; IG_C1.
InterPro; IPR00359; IG_WC.
InterPro; IPR00359; IG_WC.
InterPro; IPR00359; IG_WC.
InterPro; IPR00459; IG_WC.
INTERPRO; IRR0409; IG, 2.
SWART; SW00409; IG, 2.
SWART; SW00409; IG, 2.
PR0SITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences."
                                                                                                                                                                                               QGGMX1 HUMAN PRELIMINARY;
QGGMX1;
                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
Homo sapiens (Human).
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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                                62
                                                                                                                                                                              HUMAN
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Attaubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Riaunner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Raplaton M., Soares M.B., Bonaldo M.F., Casrainci P., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
T. "Generation and initial analysis of more than 15,000 full-length human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                              Hypothetical protein.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                                                                                                         [1]
NUCLECTIDE SEQUENCE.
TISSUE=Primary B-Cells;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73.8%; Score 462.5; DB 2; Length 477; 77.5%; Pred. No. 1.8e-39; ive 9; Mismatches 13; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL: BCO73765; AAH73765.1; -; mRNA.
SMR; QGGMX7; 247-455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 477 AA; 51631 MW; 9FES9C09C50CFF85 CRC64;
05-UUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
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Matches
    SO DE RESERVE SO DE RESERVE DE RE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MCDLINE=S0067954; Pubbled=2587273;
MCDLEAUTRE=90067954; Pubbled=2587273;
MCDLINE=90067954; Pubbled=2587273;
MCDLINE=90067954; Pubbled=2587273;
MCDLEAUTRE=90067954; Pubbled=2587273;
MCDLEAUTRE=1006195 against porcine transferrin.";
MCDLEAUTRE=17:9481-9481(1989).
MCDLEAUTRE=17:9481-9481(1989).
MCDLEAUTRE=17:9481-9481(1989).
MCDLEAUTRE=17:9481-9481(1989).
MCDLEAUTRE=17:9481-9481(1989).
MCDLEAUTRE=17:9481-9481(1989).
MCDLEAUTRE=18:9481-9481(1989).
MCDLEAUTRE=18:9481(18:9481-9481(18:9481).
MCDLEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 PSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCAR-YGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 PSLKORISITRDISKNQFPLKLNSVTTEDTATYYCTRGDGYHFFTYWGGGTLVIVSA 136
                                                                                                                   Mus musculus (Mouse).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
20 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQTAGKGLEWIGYISHSGSTTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNYK
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72.6%; Score 455.5; DB 2; Length llarity 72.6%; Pred. No. 2.5e-39; Conservative 14; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136 AA; 15307 MW; 5B0F439CCFB15C3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
VH gene product (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                    136 AA
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                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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PROSITE; PS50835; IG LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                           QGLBQS_MOUSE PRELIMINARY;
QGLBQS;
05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 MOUSE
Q5U413 MOUSE PRELIMINARY;
Q5U413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
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nes 85; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOC544903 protein.
Name=LOC544903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON TER
SEQUENCE
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Statchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Caarvant T.L., Scheetz T.E., Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Rogak S.A., McEwann P.J., Malek J.A., Ganziarathe P.H., Richards S., Worley K.C., Hale S., Garcia A., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Parky J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Rokriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., M. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (tuman).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
"Clonal proliferation of IgM secreting B cell in the synovium of Behcet's patient with arthritis.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
[2]
NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, BC085312, AAH85312.1; mRNA.

Ensembl; ENSWUSG000054328; Mus musculus.

GO; GO:00030359; Enantigen binding; IEA.

InterPro; IPR003599; Ig.

InterPro; IPR003599; Ig.

InterPro; IPR003597; Ig.

InterPro; IPR003596; Ig.

InterPro; IPR003596; Ig.

InterPro; IPR003596; Ig.

InterPro; IPR003596; Ig.

InterPro; IPR004096; Ig. 3.

SNART; SM00409; IG. 3.

SNART; SM00406; IGV; 1.

REAL; PROSITE; PS00399; IG LIKE; 4.

REQSITE; PS00399; IG LIKE; 4.

REQSITE; PS00399; IG MHC; UNKNOWN 2.

SRQUENCE 483 AA; $\begin{array}{c}

STATT AMP; TC272DASO1A4AOD1 CRC64;

SEQUENCE 483 AA; $\begin{array}{c}

STATT AMP; TC272DASO1A4AOD1 CRC64;

STATT AMP; TC272DASO1A4AOD1 CRC64;
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Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
VH4 heavy chain variable region precursor (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-FVB/N; TISSUE-Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        095973_HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.
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(2)
NUCLEOTIDE SEQUENCE
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HV46_MOUSE
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RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
REDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RIALINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altechul S.F., Zeeberg B. Buctow K.H., Schaefer C.F., Bhat N.K.,
RA HOpkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Diatchenko L., Gares M.B., Doshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Weckernan K.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Marcia M.A., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Buteerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.N.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.N.,
Rand Mouse CDNA Sequences.,

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                       Harindranath N., Goldfarb I.S., Ikemateu H., Buraetero S.E.,
Wilder R.L., Nockins A.L., Casali P.;
Wilder R.L., Nockins A.L., Casali P.;
"Complete sequence of the genes encoding the VH and VL regions of low-
"Complete sequence of the genes encoding the VH and VL regions of low-
"T and high-affinity monoclonal 18A1 rheumatoid factors produced
"I Int. Immunol. 3:865-875(1991).
"I Embl. AF103795; ARC79084.1; -; mRNA.
"R EMBL, AF103795; ARC79084.1; -; mRNA.
"R PIR; 531673; S31673.
"R HSSP: PO1820; 1G7J.
"R HSSP: PO1820; 1G7J.
"R InterPro; IPR001596; 1G-
"I InterPro; IPR001596; 1G-
"I InterPro; IPR001596; 1G-
"I INTERPRO; IRR SMORT; SMOR406; 1G-
"R PROSITE; PSS0835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLQESGPGLVKPSETLSLTCTVSGYSITG-GYLWNWIRQPPGKGLEWIGYISYDGTNN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 QLQLQESGPGLVKPSETLSLSCTVSGGSISSTNYYWGWIRQPPEKGLEWIGSLHNSGSDY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 YNPSLKSRVTISVDTSKNOFSLRLSSVTAADTAVYYCARLGMGAFDFWGHGTMVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 YKPSLKORVTISRDTSKNQPSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VH4 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.5%; Score 454.5; DB 2; Length 75.4%; Pred. No. 3.5e-39; ive 9; Mismatches 19; Indels
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Potential.
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QEP418;
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Matches 89; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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61 KPSLKDRVTISRDTSKNOFSLKLSSVTAADTAVYYCARYGRVFF---DYWGQGTLVTVSS 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIJINE-89238351; PubMed-2497341; DOI=10.1016/0161-5890(89)90133-8; Rinfret A., Horne C., Dorrington K.J., Klein M.; "Cloning, sequencing and expression of the rearranged MOPC 315 VH gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 QVQLQESGPGLVKPSGTLSLTCAVSGGSISSSNWWSWVRQPPGKGLEWIGEIYHSGSTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
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Schechter I., Wolf O., Zemell R., Burstein Y.;
"Structure and function of immunoglobulin genes and precursors.";
Fed. Proc. 38:1839-1845(1979).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 576;
                                                                                                                                                                                                                                                                                    InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003100; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
InterPro; IPR0047; Ig_V.
InterPro; IPR00407; Ig_V.
InterPro; IPR00409; IG_I.
InterPro; IPR00407; Ig_V.
InterPro; IPR00409; IG_I.
InterPro; IPR00409; Ig_I.
InterPro; IPR0417; Ig_V.
InterPro; IPR0417; IRR; InterPro; IPR0417; IRV0417; Ig_V.
IPR0417; IRV0417; Ig_V.
IPR0417; IRV0417; Ig_V.
IRV0417; IRV0417; IRV0417; Ig_V.
IRV0417; IRV0417; IRV0417; Ig_V.
IRV0417; IRV0
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                                         Strausberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC063184; AAH63184.1; -; mRNA.
HSSP; P01820; 1A7N.
Ensembl; ENSG0000196122; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 454.5; DB 2;
Pred. No. 1.6e-38;
8; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696(1977).
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01-AVG-1992 (Rel. 23, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
1g heavy chain V region MOPC 315 precursor.
Mus musculus (Mouse).
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MEDLINE=78094475; PubMed=414225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Muroidea; Muridae; Murinae; Mus
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TISSUE=Primary B-Cells;
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NCBI_TaxID=9606;
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                                                                                                                            This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNYK 61
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                       MEDLINE=77244979; PubMed=268248;
Hood L., Margolies M.N., Givol D., Zakut R.;
Unpublished results, cited by:
Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;
Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).
-!- MISCELLANEOUS: This alpha chain was isolated from a myeloma protein that has anti-dinitrophenyl activity.
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                                                                                                                                                                                                                                                                                                                                        chain V region MOPC 315.
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By similarity.
G -> GG (in Ref. 1; CAA30727).
G -> H (in Ref. 2).
G -> H (in Ref. 4).
N -> D (in Ref. 4).
Missing (in Ref. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.4%; Score 454; DB 1; Length 137; 71.2%; Pred. No. 3.6e-39; ive 14; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                              Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                                                                                                    Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                                                                                       Complementarity-determining-3
a mouse myeloma protein with anti-hapten activity.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                  SWART; SW00406; IGV; 1.—
PROSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region; Signal.
           Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974)
                                                                                                                                                                                            EMBL; M27638; AAA61337.1; -; Genomic_DNA.
EMBL; X07880; CAA30727.1; -; Genomic_DNA.
HSSP; P0102; AVMS35.
HSSP; P01820; 1G7J.
SMR; P01822; 20-137.
Ensembl; EMSWUSGO000057048; Mus musculus.
InterPro; IPR007110; IG-1ike.
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Matches 84; Conservative
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68
68
1116
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                              SEQUENCE REVISION TO
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123
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137 AA;
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Name=IGHM;
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Neale G.A., Kitchingman G.R.;
"mRNA transcripts initiating within the human immunoglobulin mu heavy chain enhancer region contain a non-translatable exon and are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
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PROSITE; PS00290; IG MHC; UNKNOWN 3.
SEQUENCE 620 AA; 60125 MW; 990A1A4A6E8FF27B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             extremely heterogeneous at the 5' end."; unclaic Acids Res. 19:2427-2433(1991). EMBL; BC011857; AAH11857.2; -; mRNA. PIR; S15590; 815590.
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SWR; Q96EY0; 27-251.
Ensembl; ENSG00000130076; Homo sapiens.
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InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-cl.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_w.
Pfam; PF07654; Cl-set; 4.
SMART; SM00409; IG; 2.
SMART; SM00407; IGcl; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.
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Matches 93; Conservative
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TISSUE-Primary B-Cells;
FISSUE=Primary B-Cells;
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 8 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 VQLQESGPGLVKPSQSLSLTCSVTGYSITSGYYWNWIRQFPGNKLEWMGYISYDGSHNYN 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 PSLKDRVTISRDTSKNOFSLKLSSVTAADTAVYYCA----RYGRVFF---DYWGQGT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 PSLKORISITRDTSKNQPFLKLNSVTIEDTATYYCARPLYYRYDEEYYYAMDYWGQGT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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TISSUE=Human rectum tumor;

TISSUE=Human rectum tumor;

A Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,

R Bloecker H., Boecher M., Miemann S.;

L Submitted (JUN-2003) to the EWBL/GenBank/DDBJ databases.

E EMBL; BX530666; CAD97996.1; -; mRNA.

R EMBL; BX530666; CAD97996.1; -; mRNA.

R EMBL; BX5000000130076; Homo sapiens.

R InterPro; IPR00310; Ig-dl.

R InterPro; IPR03597; Ig_cl.

R InterPro; IPR03597; Ig_cl.

R InterPro; IPR03596; Ig_MC.

R InterPro; IPR03596; Ig_MC.

R InterPro; IPR03596; Ig_WC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
"The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic) antibodies in the GAT system.";
EMBO J. 4:3681-3688(1985).
                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fougereau M.;
Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
EMBL; X03378; CAA27095.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 AA; 13931 MW; 502E51A5213F056E CRC64;
                                                                                                                                                                     13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
VH-D-JH region (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp686K04218 (Fragment).
Name=DKFZp686K04218,
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 71.3%; Score 447; DB 2; Best Local Similarity 70.3%; Pred. No. 1.6e-38; Matches 83; Conservative 14; Mismatches 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 478 AA
                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
MEDLINE=86136012; PubMed=3937730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE OF 28-29.
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Q72379;
                                                                                                        QS3VQS_MOUSE PRELIMINARY;
QS3VQS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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                                RESULT 12
053V05 MOUSE
053V05 MOUSE
DT 13-SEP-20
DT 13-SEP-20
DE WH-D-JH 19
DE WH-D-JH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
Q7Z379_HUMAN
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60 YKPSLKDRVTISRDTSKNOFSLKLSSVTAADTAVYYCAR---YGRVFFDYWGQGTLVTVS 116
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2004 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKPZp686C0218 (Fragment).
Name-DKFZp686C02218;
Homo saplens (Human)
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUB-Human rectum tumor;
Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
L. Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
BMBL; BX538077; CAD98001.1; -; mRNA.
BMSP; PO1820; 1G7J.
BMSP; PO1820; 1G7J.
BRSP; PRO03596; 1G7J.
BRSP; PRO0406; 1GV; 1.
BROSITE; PS50835; 1G LIKE; 4.
BROSITE; PS50835; 1G LIKE; 4.
BROSITE; PS50835; 1G LIKE; 4.
BROSITE; PS00290; 1G LIKE; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 OVOLOESGPGLVKPSETLSLTCTVSGYSITG-GYLWNWIRQPPGKGLEWIGYISYDGTNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 QVQLQESGPGLVKPSQTLSLTCTVSGGSIGSGDYFWSWIRQAPGRGLEWMGYIYYSGSTY
                                                                                                                                                                                                                                                                                                                                                                                          1 QVQLQESGPGLVKPSETLSLTCTVSGYSI-TGGYLWNWIRQPPGKGLEWIGYISYDGTNN
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                   Length 478;
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1 Similarity 72.4%; Pred. No. 6.8e-37;
89; Conservative 8; Mismatches 18; Indels
                                                                                                                                                                                                                                                Match 70.1%; Score 439.5; DB 2; Length Local Similarity 71.9%; Pred. No. 4.6e-37; Length 87; Conservative 14; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;
                                                                                                                                                                                478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   492 AA
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
Hypothetical protein.
1 1
SEQÜENCE 478 AA; 51620 MW; 4AFCB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q72374 HUMAN PRELIMINARY;
Q72374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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150 VSS 152

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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MR-2004 (TrEMBLrel. 26, Last amotation update)
01-MR-2004 (TrEMBLrel. 26, Last amotation update)
Full-Length cDNA clone GSOBLO04YM19 of B cells (Ramos cell line) of Homo sapiens (Human) (Fragment).
Homo sapiens (Human) (Pragment).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 69.3%; Score 434.5; DB 2; Length 139; Best Local Similarity 86.7%; Pred. No. 3.9e-37; Matches 85; Conservative 3; Mismatches 9; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genoscope;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX248300; CAD62627.1; -; mRNA.
HSSP; PO1820; 1G7J.
SNR; Q86SX2; 33-129.
Ensembl; ENSG90000130076; Homo sapiens.
InterPro; IPR007110; 1g-1ike.
InterPro; IPR00710; 1g-1ike.
SNART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
TISSURE acula;
Li W.B., Gubarer C., Jessee J., Polayes D.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 139 AA; 15573 MW; 7D1E2302410E4F8C CRC64;
                                                                                                 139 AA
                                                                                                 PRT;
                                                                                             Q86SX2_HUMAN PRELIMINARY;
Q86SX2;
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TISSUE=B cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo.
NCBL_TaxID=9606;
                                                       HUMAN
RESULT 15
0865XZ HUM
10 0066XX
AC 0865X
AC 0865X
AC 0865X
DT 01-JU
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92 NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR 129

61 KPSLKDRVTISRDTSKNOFSLKLSSVTAADTAVYYCAR 98

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Search completed: January 10, 2006, 20:53:27 Job time : 78.8731 secs

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January 10, 2006, 20:07:41; Search time 80.7649 Seconds (without alignments) 636.505 Million cell updates/sec
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GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                            protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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geneseqp2001s:*
geneseqp2003s:*
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length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Adj76913 Anti-IGP-Adz67083 Human ant Adj76915 Anti-IGF-Adz67079 Human ant Adj76919 Anti-IGF-Adz67079 Human ant Adj76919 Anti-IGF-Adz67089 Human ant Adj76919 Anti-IGF-Adz67089 Human ant Adj76919 Anti-IGF-Adz67089 Human ant Adj76903 Anti-IGF-Adz67089 Human ant Adj76903 Anti-IGF-Adz67056 Murine im Adj76903 Anti-IGF-Adz67056 Murine im Adj76896 Anti-IGF-Adz67056 Humanised Adg16559 Humanised Adg16559 Humanised Adg16559 Humanised Adg16898 Murine-ex Adp03889 Murine-ex Adp03889 Murine-ex Human ant Anti-IGF-Human ant Anti-IGF-Human ant Anti-IGF-Human ant Anti-IGF-Human ant Humanised Murine-ex Murine-ex Murine im Murine im Human ant Humanised Murine-ex Humanised SUMMARIES ADZ67083 ADZ67083 ADZ67085 ADZ67079 ADZ67079 ADZ67081 ADZ67081 ADZ67087 ADC27457 AAY15126 ADP03973 ADC27455 ADS16559 Query Match Length DB 1117 135 135 117 541 509.5 509.5 504.5 506.5 506.5 503.5 503.5 Score 627 627 627 623 623 623 623 615 615 615 615 615 615 Result Š.

Adp03958 Murine-ex	_	Abb07171 ebvHigM M	Adi26658 Human ant	Adp03887 Murine-ex	Adp03884 Murine-ex		Abj18676 Antibody		Ade28479 Human ant	Ady74798 Human IgG	Human	Ade28491 Human ant		Aao30915 dI-NHS76	Aao30913 dI-NHS76	Aea21456 Human ant	Adx98267 Human ant	Ads16505 Human ant	Ads16613 Human ant	Ade28447 Human ant
ADP03958	ADP03957	ABB07171	AD126658	ADP03887	ADP03884	AAW27554	ABJ18676	ADE28455	ADE28479	ADY74798	AAY44615	ADE28491	ADE28471	AA030915	AA030913	AEA21456	ADX98267	ADS16505	ADS16613	ADE28447
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120	116	121	121	122	122	119	119	121	466	119	117	121	466	580	580	122	139	121	169	121
80.1	79.8	79.8	79.8	79.8	79.8	79.7	79.7	79.7	79.7	79.4	79.3	79.3	79.3	79.3	79.3	79.0	79.0	78.9	78.9	78.8
502.5	500.5	500.5	500.5	500.5	500.5	200	200	200	200	498	497	497	497	497	497	495.5	495.5	494.5	494.5	494
25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	4	41	42	43	44	45

## ALIGNMENTS

cytostatic; antipsoriatic; antibody; insulin-like growth factor-1 receptor; IGF-IR; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region; New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers. (FABR ) FABRE MEDICAMENT SA PIERRE. ADJ76913 standard; protein; 117 AA Anti-IGF-1R related protein #24. Leger 0; 20-JAN-2003; 2003WO-FR000178. 18-JAN-2002; 2002FR-00000653. 18-JAN-2002; 2002FR-00000654. 07-MAY-2002; 2002FR-00005753. (first entry) Corvaia N, WPI; 2003-569653/53. WO2003059951-A2 Ношо варіепв. 06-MAY-2004 24-JUL-2003. Goetsch L, ADJ76913; RESULT 1 ADJ76913 

Disclosure; SEQ ID NO 79; 164pp; French

The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of

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these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGP-IR and/or EGPR. This sequence represents a protein sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; heavy chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
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100.0%; Pred. No. 1.8e-48;
iive 0; Mismatches 0;
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07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WO-FR000178.
11-JUL-2003; 2003FR-00006538.
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Matches 117; Conservative
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CORVAIA N.
LEGER O.
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18-JAN-2002; 2
07-MAY-2002; 2
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The inversion relates to a novel isolated anti-insularity being capable of binding to human IGF-IR and, if necessary, capable of capable of binding to human IGF-IR and, if necessary, capable of capable of binding tromaine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or connected with a cativation of the IGF-IR and/or EGFR, and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly induced intended of the antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral capendary effects connected with inhibitions of the insulin receptor. The antibody is useful for preparation of a medicament intended to inhibit the graparation of a medicament and/or EGF-dependent and/or EGF-dependent and/or HER2/neu-dependent and/or IGF2-dependent and/or IGF2-dependent and/or IGF2-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent cells. (I) is useful in the preparation of a medicament intended for prevention or for the treatment of psoriasis. (I) is useful in the preparation of a medicament intended for the special or the preparation of a medicament intended for the preparation of a medicament intended for the specific targeting of a biologically active compound to intended for the specific targeting of a biologically active compound to intended for the specific targeting of a biologically active compound to intended for the specific targeting of inten
novel isolated anti-insulin-like growth factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is useful for in vitro quagnosis or this case, conversed or despect overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF entiting from a manner of enemanted. Which involves contacting the
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100.0%; Pred. No. 1.8e-48;
iive 0; Mismatches 0;
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Goetsch L,

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Agentation of the transduction pathway of the signal mediated by the interaction of the transduction pathway of the signal mediated by the interaction of the transduction pathway of the signal mediated by the interaction of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral character, preferably 1GF-dependent, especially IGF1 and/or 1GF2-dependent and/or HERZ/neu-dependent cells. [I) is useful for preparation of a medicament intended to inhibit the growth capecially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or IGF2-dependent and/or IGF2-dependent and/or IGF2-dependent and/or IGF3-dependent cells. [I) is useful in the preparation of a medicament intended for prevention or for the treatment of cancer, where the cancer is chosen from prostate cancer, osteosarcom, lung cancer, breast cancer, endometrial cancer or colon cancer. [I) is useful in the preparation of a medicament intended for the specific targeting of a biologically active compound to cells expressing or overexpressing the IGF-IR and/or EGFR receptor. [I] is useful for in vitro diagnosis of illnesses induced by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (I), which is optionally labeled. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting to kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or connected with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
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69. .84
/note= "CDR2"
117. .124
                                                                            /note= "CDR3"
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07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WO-FR000178.
11-JUL-2003; 2003FR-00008538.
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CORVAIA N.
LEGER O.
DUFLOS A.
HAEUW J.
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(DUFL/)
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     Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with these receptors with their ligands. Bspecially they inhibit transformation of normal cells, so are useful against cancers of the proliferation of tumor cells, so are useful against cancers of the prostate. Jung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are a slo used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a
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                                                                                                                                                                                                                                                                                                                 New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 627; DB 7; Length 135; 100.0%; Pred. No. 2e-48; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein sequence used to generate the Ab of the invention
                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 81; 164pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .18
/note= "leader peptide"
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                                                                                                                                                         (FABR ) FABRE MEDICAMENT SA PIERRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADZ67085 standard; protein; 135 AA.
                                                                                                                                                                                                           Corvaia N, Leger O;
                                                                          18-JAN-2002; 2002FR-0000654.
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20-JAN-2003; 2003WO-FR000178
                                                      18-JAN-2002; 2002FR-00000653
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Matches 117; Conservative
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Query Match

δ 셤 ò 셤 Homo sapiens.

Peptide Region

30-JUN-2005

ADZ67085;

RESULT 4 ADZ67085

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Mismatches

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                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                               insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                              78
                                                                                                                                                                61 KPSLKDRVTISRDTSKNQPSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                       79 KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                               19 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                         QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
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                     Length 135;
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                                                       Indels
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                 Score 627; DB 9;
Pred. No. 2e-48;
100.0%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                cytostatic; antipsoriatic; antibody;
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18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-00005753.
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                                                       Matches 117; Conservative
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                                      Best Local Similarity
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                     Query Match
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Score 623; DB 7; Length 117; Pred. No. 4e-48;

99.4%;

Query Match Best Local Similarity

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Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obsterrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; periasis; dermatological disease; immune disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel isolated anti-insulin-like growth factor a receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tyrosine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined if amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal hyperactivation of the IGF-IR and/or EGFR, and/or connected with a hyperactivation of the transduction pathway of the signal mediated by the interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
                                                                 KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                  KPSLKDRITISRDTSKNOFSLKLSSVTAADTAVYYCARYGRVFFDYWGGGTLVTVSS 117
                             QVQLQESGPGLVKPSETLSLTCTVSGYS1TGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                                                                                      Human antibody 7C10 1 heavy chain variable region SEQ ID NO:75.
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                                                                                                                                                                                     ADZ67079 standard; protein; 117
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07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WO-FR000178.
11-JUL-2003; 2003FR-00008538.
                                                                                                                                                                                                                                                                                                                                                                                                                              chain variable region.
                                                                                                                                                                                                                                                      (first entry)
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CORVAIA N.
LEGER O.
DUFLOS A.
HAEUW J.
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(LEGE/)
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(HAEU/)
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sequence is used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                 Anti-IGF-1R related protein #23.
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07-MAY-2002; 2002FR-00005753.
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                                                                                                                                                                                                                                                                                                    (first entry)
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Best Local Similarity 98.3
Matches 115; Conservative
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                                                                                                                                                            Sequence 117 AA;
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fragments, that bind to human insulan-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulan-like growth factor-1 receptor (IGF-IR) and optionally: (ii) inhibit natural binding of insulan-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or considerated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with the insulant in their ligands. Especially they inhibit cransformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention. Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; KPSLKDRVIISRDISKNQPSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117 KPSLKDRITISRDISKNQPSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 135 New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers. QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY Human antibody 7C10 1 heavy chain variable region SEQ ID NO:77. 99.4%; Score 623; DB 7; Length 135; 98.3%; Pred. No. 4.7e-48; ive 2; Mismatches 0; Indels Disclosure; SEQ ID NO 77; 164pp; French 1. .18 /note= "leader peptide" Location/Qualifiers ADZ67081 standard; protein; 135 AA 69. .84 /note= "CDR2" 117. .124 /note= "CDR3" 49. .54 /note= "CDR1" 16-DEC-2003; 2003US-00735916 18-JAN-2002; 2002FR-00000653 heavy chain variable region. (first entry) Best\_Local Similarity 98.3 Matches 115; Conservative Sequence 135 AA; US2005084906-A1 Homo sapiens 30-JUN-2005 21-APR-2005. Н 61 ADZ67081; 13 Query Match Peptide Region Region Region ADZ67081 RESULT ઠે 셤 ઠે a the administration of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin creceptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral chemacier, preferably IGF-dependent, especially IGF1 and/or IGF2-CC dependent and/or ERZ/neu-dependent cells. (I) is useful for preparation of tumor cells, preferably IGF-dependent, or especially IGF1 and/or IGF2-dependent and/or cells, preferably IGF-dependent, cells, is useful in the preparation of a medicament intended for prevention or for the treatment of cancer, che cancer, obteosarcoma, lung cancer, che cancer, endometrial cancer or colon cancer. (I) is useful in the preparation of a medicament intended for the prevention or for the treatment of psoriasis. (I) is useful in preparation of a medicament cinended for the special or or verexpressing or overexpressing the IGF-IR and/or EGFR receptor is useful for in vitro diagnosis of illnesses induced by an overexpressing or an underexpression of the IGF-IR and/or EGFR receptor is tarting from a biological sample with the abnormal present of proposical sample with involves contacting the invarior of proposical sample with involves contacting the present invalves contacting the invalves contacting the present invalves contacting the invalves contacting the present invalves contacting the present invalves contacting the contacting the present invalves contacting the contacting the present invalves contacting the present invalves contacting the ö 9 insulin-like growth factor-1 receptor; IGF-IR; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region; QVQLQESGPGLVXPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY 60 61 KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117 61 KPSLKDRITISRDTSKNOPSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117 0; Gaps Score 623; DB 9; Length 117; Pred. No. 4e-48; 2; Mismatches 0; Indels

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Gaps

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ADJ76917 standard; protein; 117 AA

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The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting to have activity of the receptor, capable of specifically inhibiting tyroshine kinase activity of the receptor, of specifically inhibiting tyroshine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADS67006 and ADS67014). An antibody of the invention is useful in a cativation of a medicament intended of the preraction of a medicament intended of an illness connected with an overexpression and/or a bnormal colf an illness connected with IGF-IR and/or CGF at illness connected with IGF-IR and/or GFF with EGFW, where contraction of the IGF-IR and/or EGFW, and/or of EGF with EGFW, where interaction of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended to inhibit the preparation of a medicament intended to inhibit the growth capecially IGF-dependent and/or EGF-dependent of a medicament intended for prevention of the preparation of a medicament intended for prevention or for the treatment of general endometrial cancer or colon cancer. (I) is useful in the preparation of a medicament intended for the presention of a medicament intended for the presention of a medicament intended for the specific targeting of a biologically active compound to the specific targeting of a medicament intended for the specific targeting of the IGF-IR and/or EGFR receptor. (I) is useful for in vitro diagnosis of illnesses induced to the specific targeting the IGF-IR and/or EGFR receptor is useful for in vit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
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2; Mismatches
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                                  07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WO-FR000178.
11-JUL-2003; 2003FR-00008538.
2002FR-00000654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful for treating cancer.
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CORVAIA N.
LEGER O.
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18-JAN-2002;
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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF-IR) and/or -2; and/or (ii) inhibit specifically tyrosine chinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (IGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit contains formation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteoaarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused to by abnormal expression of IGF-IR and/or EGFR. This sequence represents a
                                                                                                                                 insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity, or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region; CDR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein sequence used to generate the Ab of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (FABR ) FABRE MEDICAMENT SA PIERRE.
                                                                                             Anti-IGF-1R related protein #26.
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07-MAY-2002; 2002FR-00005753
                                                     06-MAY-2004 (first entry)
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                                                                                                                                                                                                                                                                                       WO2003059951-A2.
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                 ADJ76917;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inceptor (IGF-IR) antibody (I) of its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tyrosine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or connected with a cativation of the IGF-IR and/or BGFR, and/or of EGF with BGFR, where interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with BGFR, where the administration of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin receptor, The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells with tumoral character, preferably IGF-dependent, especially IGF1 and/or IGF2.
                                                                                                                                                                                                           neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriaais; dermatological disease; immune disorder; heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel isolated anti-insulin-like growth factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
                                                                                                                                                                                            Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
                                                                                                                                                 Human antibody 7C10 3 heavy chain variable region SEQ ID NO:83.
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                      ADZ67087 standard; protein; 117 AA.
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18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-00005753.
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11-JUL-2003; 2003FR-00008538
                                                                                                         (first entry)
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CORVAIA N.
LEGER O.
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HAEUW J.
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(HAEU/)
(BECK/)
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preparation of a medicament intended for the prevention or for the preparation of a medicament intended for the prevention or for the inteadment of pagralasis. (1) is useful in preparation of a medicament intended for the specific targeting of a biologically active compound to cells expressing or overexpressing the IGF-IR and/ox EGFR receptor. (1) is useful for in vitro diagnosis of illnesses induced by an overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (1), which is optionally labeled. The present sequence is used in the exemplification of the invention.
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98.3%; Pred. No. 2.1e-47;
iive 1; Mismatches 1;
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07-MAY-2002; 2002FR-00005753.
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Matches 115; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 117 AA;
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           these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteoparcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder;
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hyperactivity of Bignal transduction pathways mediated by interaction of
                                                                                                                                                                                                                                                              61 KPSLKDRVTISRDTSKNQPSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                              KPSLKDRVTISVDTSKNOFSLKLSSVTAADTAVYYCARYGRVFPDYWGQGTLVTVSS 135
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                                                                                                                                                     Score 615; DB 7;
Pred. No. 2.4e-47;
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/note= "CDR1"
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/note= "CDR2"
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/note= "CDR3"
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2002FR-00005753.
2003WO-FR000178.
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98.3%;
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Best Local Similarity 98.3
Matches 115; Conservative
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/note=
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CORVAIA N.
LEGER O.
DUFLOS A.
HAEUW J.
BECK A.
                                                                                                                          Sequence 135 AA;
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The invention fraction to a note; isolated anti-insulin-like growth factor is expecifically inhibiting tyrosine kinase activity of the receptor.

Compable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tyrosine kinase activity of the receptor.

Comparising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal consistion of the IGF-IR and/or EGFR, and/or of EGF with EGFR, where the administration of the ransduction pathway of the signal mediated by the induces secondary effects connected with inhibition of the insulin creceptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral character, preferably IGF-dependent, especially IGF-dependent and/or EGF-dependent and/or HER2/neu-dependent and/or IGF2-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent cells, preferably IGF-dependent cells, preferably IGF-dependent cells.

CC HER2/Ineu-dependent cells. (I) is useful in the preparation of a medicament intended for prevention or for the treatment of psoriasis. (I) is useful in preparation of a medicament intended for the specific targeting of a biologically active compound to the subsection of a medicament intended for the specific targeting of a biologically active compound to the subsection of a medicament intended for the specific targeting of a biologically active compound to the subsection of a medicament intended for the specific targeting of a biologically active compound to the subsection of a medicament of psoriasis of illnesses induced by an overexpressing or the preparation of a medicament of subsection of a medicament of subse
                                                                                                                                                                                                                                                                            The invention relates to a novel isolated anti-insulin-like growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a blological sample in which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (I), which is optionally labeled. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                              Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLMNWIRQPPGKGLEWIGYISYDGTNNY 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 KPSLKDRVTISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KPSLKDRVTISVDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
Beck A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
     Haeuw J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 615; DB 9;
Pred. No. 2.4e-47;
1; Mismatches 1;
Duflos A,
                                                                                                                                                                                                                            Example 13; SEQ ID NO 85; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic; antipsoriatic; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADJ76903 standard; protein; 117 AA
  Leger O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-IGF-1R related protein #16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98.1%;
                                                                                                                                                                         cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 98.3
Matches 115; Conservative
Corvaia N,
                                              WPI; 2005-321968/33.
                                                                                                                                                                         useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-MAY-2004
  Goetsch L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADJ76903;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
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fragments, that bind to human insulin-like growth factor-1 receptor (IGP-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, on are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating specials. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; BGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murine immunoglobulin heavy chain variable region 7C10 VH SEQ ID NO:69
                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention relates to an isolated antibody (Ab), and its functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLMNWIRQFPGNKLEWMGYISYDGTNNYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSLKDRVTISRDTSKNQPSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86.3%; Score 541; DB 7; Length 117; 84.5%; Pred. No. 9e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 69; 164pp; French
                                                                                                                                                                                                                                                                                                                                     (FABR ) FABRE MEDICAMENT SA PIERRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADZ67073 standard; protein; 117 AA.
                                                                                                                                                                                                                                                                                                                                                                            Leger 0;
                                                                                                                                                                                                                                                                            18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
                                                                                                                                                                                                                   20-JAN-2003; 2003WO-FR000178
                                                                                                                                                                                                                                                          18-JAN-2002; 2002FR-00000653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 84.5%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JUN-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                                              Corvaia N,
                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-569653/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 117 AA;
                                                                                                                                      WO2003059951-A2.
                        or epidermal
                                                                                                   Homo sapiens.
                                                                                                                                                                          24-JUL-2003
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contraction of the transduction pathway of the signal mediated by the interaction of 1GF1 or 1GF2 with IGF-IR and/or of EGF with EGFR, where the administration of the medicament does not induce or only alightly induces secondary effects connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral caracter, preferably IGF-dependent, especially IGF1 and/or IGF2.

C dependent and/or EGF-dependent, especially IGF1 and/or IGF2.

C dependent and/or EGF-dependent and/or HERZ/neu-dependent cells. (I) is useful for preparation of tumor cells, preferably IGF-dependent, cepscially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or EGF-depen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tyrosine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADS-6006 and ADS-67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or connected with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; immunoglobulin; heavy chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Duflos A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 13; SEQ ID NO 69; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leger O,
                                                                                                                                                                                                                                                                                                                 18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WO-FR000178.
11-JUL-2003; 2003FR-00008538.
                                                                                                                                                                                                                                                16-DEC-2003; 2003US-00735916
                                                                                                                                                                                                                                                                                                2002FR-00000653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corvaia N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2005-321968/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                        GOETSCH L.
CORVAIA N.
LEGER O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DUFLOS A. HAEUW J.
                                                                                                                                                  US2005084906-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BECK A.
                                                                                                                                                                                                                                                                                                .8-JAN-2002;
                                                                                                       Mus musculus.
                                                                                                                                                                                                  21-APR-2005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Soetsch L,
                                                                                                                                                                                                                                                                                                                                                                                                                                             (GOET/)
(CORV/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (LEGE/)
(DUFL/)
(HAEU/)
(BECK/)
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Sequence 117 AA;

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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth actors (IGF) - and/or (ii) inhibit specifically tyrosine (IGF) - and/or 1. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with these receptors with their ligands. Bepecially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or prostate, lung, breast, endometrium and colon, also osteosarcome, and also for treating psoriasis. Ab are also used to diagnose diseases caused to be abnormal expression of IGF-IR and/or EGFR. This sequence represents a content of the interval of the interval or content or content.
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                                                                             2 VOLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNYK 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                  2 VQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQPPGNKLEWMGYISYDGTNNYX
                                                                                                                                                           62 PSLKDRVTISRDTSKNOFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                62 PSLKDRISITRDISKNOFFLKLNSVINEDTATYYCARYGRVFFDYWGGGTTLIVSS 117
                                         Gaps
                                         ö
Length 117;
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                                         8; Indels
86.3%; Score 541; DB 9;
84.5%; Pred. No. 9e-41;
                                      98; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 52; 164pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytostatic; antipsoriatic; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (FABR ) FABRE MEDICAMENT SA PIERRE.
                                                                                                                                                                                                                                                                                                   ADJ76886 standard, protein; 127 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-IGF-1R related protein #4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JAN-2002; 2002FR-00000653.
18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
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                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 127 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003059951-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus,
                                                                                                                                                                                                                                                                                                                                                                               06-MAY-2004
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Query Match
                                         Matches
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Score 541; DB 7; Length 127; Pred. No. 9.8e-41;

86.3%;

Query Match Best Local Similarity

Search completed: January 10, 2006, 20:44:17 Job time : 80.7649 secs

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72.
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628
1 QVQLQESGPGLVKPSETLSL.......RYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published Applications AA_New:*

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

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                             GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61141 seqs, 8493638 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                 Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                  Run on:
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## SUMMARIES

	Appl	Appl	Appl	Appl	Appl	Appl	App1	Appl	, App	Appl	Appl	1, Ap	3, Ap	Appl	Appl	Appl	Appl	Appli	1619, Ap	Ä	_		, App	, App	, App
Ē	75,	77,	79,	81,	83,	85,	69	52,	162	70,	73,	1651,	1548,	34,	71,	49,	72,	ä	161	17,	1994	1329	841	112	110
Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
	3-11-012-353-75	US-11-012-353-77	US-11-012-353-79	US-11-012-353-81	US-11-012-353-83	US-11-012-353-85	US-11-012-353-69	US-11-012-353-52	ᆿ	US-11-012-353-70	US-11-012-353-73	US-11-054-515-1651	US-11-054-515-1548	US-10-512-184-34	3-10-512-184-71	3-10-512-184-49	н.	US-11-102-201-1	US-11-054-515-1619	US-10-721-763-17	US-11-054-515-1994	US-11-054-515-1329	US-11-054-515-841	US-11-054-669-112	US-11-054-669-110
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* Query Match Length	117	135	117	135	117	135	117	127	117	118	123	247	250	259	371	626	117	120	253	146	252	252	255	116	250
Query Match	100.0	100.0	99.2	99.2	97.3	97.3	86.9	86.9	84.7	77.6	76.1	76.0	76.0	75.6	75.6	75.6	74.7	74.7	74.7	74.1	73.8	73.5	73.1	72.9	72.9
Score	628	628	623	623	611	611	546	546	532	487.5	478	477.5	477.5	474.5	474.5	474.5	469	469	469	465.5	463.5	461.5	459	457.5	457.5
Result No.	1	7	e	4	S	9	7	60	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Sequence 1339, Ap Sequence 1578, Ap Sequence 1981, Ap Sequence 1981, Ap Sequence 25, Appl Sequence 21, Appl Sequence 167, Appl Sequence 167, Appl Sequence 1597, Appl Sequence 1597, Appl Sequence 55, Appl Sequence 55, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 1510, Appl Sequence 1511, Appl Sequence 1523, Appl Sequence 1231, Appl Sequence 1233, Appl Sequence 1223, Appl Sequence 1		INSULIN/IGF-I HYBRID THEREOF	Length 117; Indels 0; Gaps 0;	SYDGTNNY          SYDGTNNY	GRVFFDYMGQGTLVTVSS 117 
US-11-054-515-1339 US-11-054-515-990 US-11-054-515-990 US-11-054-515-1981 US-11-054-515-1659 US-11-054-515-1659 US-11-054-515-1670 US-11-139-499-12 US-11-139-499-12 US-11-054-515-1597 US-11-054-515-1597 US-11-164-222-20 US-11-164-222-20 US-11-054-515-1510 US-11-054-515-1510 US-11-054-515-1510 US-11-054-515-1510 US-11-054-515-1510 US-11-054-515-1510	ALIGNMENTS	ication US/11012353 1S20050249730A1 1S20050249730A1 1S20050249730A1 1S20050249730A1 1SA, NATHALIB 1SA, ALAIN 1W, ALA	;; Score 628; DB 7; ;; Pred. No. 8.7e-49; 0; Mismatches 0;	QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLMNWIRQPPGKGLEWMGYISYDGTNNY QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLMNWIRQPPGKGLEWMGYISYDGTNNY	KPSLKDRITISRDTSKNOFSLKLSSVTAADTAYYYCARYGRVFPDYWGGTLVTVSS 
72.8 253 7 72.7 254 7 72.5 251 7 72.1 254 7 71.9 154 6 71.9 254 7 70.9 256 7 70.2 251 7 70.2 251 7 70.2 253 7 70.0 259 7 70.0 259 7 70.0 259 7 70.0 259 7		2-353-75  2-75, Application US/1101235  Ation No. US20050249730A1  LINFORMATION: CONVAIA, NATHALIE CANT: CORVAIA, NATHALIE CANT: CORVAIA, NATHALIE CANT: HAEUW, JEAN-FRANCOIS CANT: LEGER, OLIVIER APPLICATION NUMBER: 10/735, 9 FILING DATE: 2003-12-16 APPLICATION NUMBER: FR 02006 FILING DATE: 2003-01-20 APPLICATION NUMBER: FR 02006 FILING DATE: 2002-01-18 FILING DATE: 2002-01-18 APPLICATION NUMBER: FR 02006 FILING DATE: 2003-01-20 APPLICATION NUMBER: FR 02006 APPLICA	100.0%; larity 100.0%; Conservative	LQESGPGLVKPSETI                LQESGPGLVKPSETI	SLKORITISRDTSKNC 
256 4 56 5 2 2 8 4 56 5 5 2 2 8 4 56 5 5 2 5 2 5 2 5 2 5 2 5 2 5 2 5 2 5		ULT 1  11-012-353-7  equence 75,  ballication here  APPLICANT:  PRICH EN PEREN  FILLE REPEREN  F	Query Match Best Local Simil: Matches 117; Co		61 KPS 
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SEQ ID NO 79
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                                                                                                                                                                                                                                             LENGTH:
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            Sequence 77, Application US/11012353
Publication No. US20050249730A1
GENERAL INFORMATION:
APPLICANT: GORTSCH, LILIANE
APPLICANT: CORTAIA, NATHALIE
APPLICANT: CORTAIA, NATHALIE
APPLICANT: DIFLOS, ALAIN
APPLICANT: BECR. ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
TILE REPERENCE: 017753-198
CURRENT APPLICATION NUMBER: 10/735,916
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: PR 0205753
PRIOR APPLICATION NUMBER: PR 020553
PRIOR PILING DATE: 2002-01-08
PRIOR PILING DATE: 2002-01-18
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Fublication No. US20050249730A1
GENERAL INFORMATION:
APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: BUECK, ALAIN
APPLICANT: BECK, OLIVIER
APPLICANT: BECK, ALAIN
APPLICANT: BECK, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
FILE REPERBENCE: 017753-198
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT PILING DATE: 2003-12-16
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: FCT/FR03/00178
PRIOR FILING DATE: 2003-07-20
PRIOR FILING DATE: 2003-01-20
PRIOR APPLICATION NUMBER: FCT/FR03/00178
PRIOR APPLICATION NUMBER: FCT/FR03/00178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-11-012-353-77
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US-11-012-353-77
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TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
FILE REPERNCE: 01753-196
FILE REPERNCE: 01753-196
FULLY APPLICATION NUMBER: US/11/012,353
CURRENT FILING DATE: 2004-12-16
FRIOR PILIATION NUMBER: R 0308538
FRIOR PILIATION NUMBER: P 03-11
FRIOR PILIATION NUMBER: P 03-11
FRIOR PILIATION NUMBER: P 03-11
FRIOR PILIATION NUMBER: P 02-11
FRIOR PILIATION NUMBER: P 02-15
FRIOR FILING DATE: 2003-03-12
FRIOR FILING DATE: 2003-03-13
FRIOR FILING DATE: 2003-03-13
FRIOR PILIATION NUMBER: P 0205753
FRIOR FILING DATE: 2002-05-07
FRIOR PILIATION NUMBER: P 0205753
FRIOR PILIATION NUMBER: P 0200653
FRIOR FILING DATE: 2002-01-18
FRIOR FILING DATE: 2002-01-18
FRIOR FILING DATE: 2002-01-18
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99.2%; Score 623; DB 7; Length 117;
Best Local Similarity 98.3%; Pred. No. 2.4e-48;
Matches 115; Conservative 2; Mismatches 0; Indels
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PRIOR FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: FR 0200653
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 0200654
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFFWARE: PatentIN Ver. 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 81, Application US/11012353;
Publication No. US20050249730A1;
GENERAL INFORMATION:
APPLICANT: CORVAIA, ILLIANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: PUBLOS, ALAIN
APPLICANT: HAEUW, JEAN-FRANCOIS;
APPLICANT: LEGER, OLIVIER
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                                                                                                                                                                                                                                                                     ; TYPE: PRT; ORGANISM: Homo sapiens US-11-012-353-79
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US-11-012-353-81
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SEQ ID NO 81
LENGTH: 135
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TYPE: PRT
CORGANISM: Homo sapiens
US-11-012-353-85
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           Sequence 83, Application US/11012353
Publication No. US20050249730A1
GENERAL INFORMATION:
APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: LEGER, OLIVIER
APPLICANT: HARUW, JEAN-FRANCIS
APPLICANT: HECK, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-OLIVIER
APPLICANT: HECK, ALAIN
TITLE OF INVENTION: NOVEL ANTI-OLIVIER
APPLICANT: APPLICANT: ALAIN
TITLE OF INVENTION: NOVER: US/11/012,353
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT FILING DATE: 2004-12-16
PRIOR FILING DATE: 2003-12-16
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-01-20
PRIOR FILING DATE: 2002-05-07
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SSOFTWARE: PRIOR PRI
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APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: LEGER, OLIVIER
APPLICANT: LEGER, OLIVIER
APPLICANT: LEGER, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
TILLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-198
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT APPLICATION NUMBER: 10/735,916
PRIOR FILING DATE: 2003-12-16
PRIOR APPLICATION NUMBER: FR 0308538
PRIOR APPLICATION NUMBER: PCT/FR03/00178
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-01-20
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Pred. No. 2.6e-47;
3; Mismatches 1.
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Publication No. US20050249730A1
GRNERAL INFORMATION:
APPLICANT: GORTSCH, LILIANE
APPLICANT: CORVAIA, NATHALIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 96.6%;
Matches 113; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT; ORGANISM: Homo sapiens
US-11-012-353-83
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US-11-012-353-85
US-11-012-353-83
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Sequence 69, Application US/11012353

Sequence 69, Application US/11012353

Publication No. US20050249730A1

GENERAL INFORMATION:

APPLICANT: GORTSCH, LILIANE

APPLICANT: CORVAIA, NATHALIE

APPLICANT: DUFLOS, ALAIN

APPLICANT: HAEW, JEAN-FRANCOIS

APPLICANT: HAEW, JEAN-FRANCOIS

APPLICANT: BECK, ALAIN

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

FRIOR FILING DATE: 2003-12-16

PRIOR FILING DATE: 2003-01-20

PRIOR FILING DATE: 2003-01-20

PRIOR FILING DATE: 2002-01-18

NUMBER OF SEQ ID NOS: 162

SEC ID NO 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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Pred. No. 1.2e-41;
8; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                         Score 611; DB 7; Length 135;
Pred. No. 3e-47;
3; Mismatches 1; Indels
PRIOR APPLICATION NUMBER: FR VEVELLY
PRIOR FILING DATE: 2002-05-07
PRIOR PELLING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARE: Patentin Ver. 3.3
SEQ ID NO 85
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Best Local Similarity 86.2%;
Matches 100; Conservative
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Best Local Similarity 96.6%;
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PRIOR FILING DATE: 2003-01-20
PRIOR PAPLICATION NUMBER: FR 0205753
PRIOR PILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: FR 0200653
PRIOR FILING DATE: 2002-01-18
PRIOR PRIOR DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARE: PATENTIN Ver. 3.3
SEQ ID NO 162
LENGTH: 117
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ORGANISM: Mus musculus
US-11-012-353-70
                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 99, Conserv
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                                                                                                                                                     Sequence 52, Application US/11012353
Fublication No. US20050249730A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: COGRECH, LILIANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: BUFLO, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANDI-IGATION NUMBER: RR 02004-12-16
PRIOR FILING DATE: 2003-01-20
PRIOR FILING DATE: 2003-01-20
PRIOR FILING DATE: 2003-01-20
PRIOR FILING DATE: 2003-01-20
PRIOR FILING DATE: 2002-01-18
PRIOR PRIOR PRIOR DATE: 2002-01-18
PRIOR PRIOR DATE: 2002-01-18
PRIOR PRIOR DATE: 2002-01-18
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Publication No. US20050249730A1

GENERAL INFORMATION:

APPLICANT: GOETSCH, LILIANE

APPLICANT: GOETSCH, LILIANE

APPLICANT: CORVALA, NATHALIE

APPLICANT: DUFLOS, ALAIN

APPLICANT: BECK, ALAIN

APPLICANT: BECK, ALAIN

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

FILE REFERENCE: 017753-198

CURRENT APPLICATION NUMBER: 10/735,916

PRIOR PLING DATE: 2004-12-16

PRIOR PPLICATION NUMBER: 10/735,916

PRIOR APPLICATION NUMBER: 10/735,916

PRIOR PLING DATE: 2003-07-11

PRIOR APPLICATION NUMBER: PCT/FR03/00178
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             62 PSLKDRISITRDTSKNQFFLKLNSVTNEDTATYYCARYGRVFFDYWGQGTTLTVSS 117
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Sequence 70, Application US/11012353
Sequence 70, Application US/11012353
Publication No. US20050249730A1
GENERAL INFORMATION:
APPLICANT: GOGTSCH, LILIANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: HEGRK, OLIVIER
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
FILING DATE: 2003-12-16
PRIOR PELICATION NUMBER: PR 0308538
PRIOR FILING DATE: 2003-01-20
PRIOR PELING DATE: 2003-01-20
PRIOR PELING DATE: 2003-01-20
PRIOR FILING DATE: 2002-01-18
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                                                                                                                                                                                                                                              1 QVQLQESGPGLVKPSETLSLTCTVSGYSISSGYYWGWIRQPPGKGLEWIGSIFHSGSSYY 60
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84.7%; Score 532; DB 7; Length 117;
84.6%; Pred. No. 2e-40;
ive 7; Mismatches 11; Indels
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77.6%; Score 487.5; I
Best Local Similarity 77.8%; Pred. No. 1.6e-
Matches 91, Conservative 10; Mismatches
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94; Conservative
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US-11-054-515-1651
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Best Local Similarity
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1 Sequence 73, Application US/11012353

1 Publication No. US20050249730A1

1 GENERAL INFORMATION:

1 APPLICANT: GORTSCH, LILIANE

2 APPLICANT: CORVAIA, NATHALIE

3 APPLICANT: CORVAIA, NATHALIE

3 APPLICANT: HAEUW, JEAN-FRANCOIS

4 APPLICANT: HEGER, OLIVIER

3 APPLICANT: HEGER, OLIVIER

4 APPLICANT: HEGER, OLIVIER

5 APPLICANT: HEGER, OLIVIER

5 APPLICANT: HEGER, OLIVIER

5 APPLICANT: HEGER, OLIVIER

6 APPLICANT: HOWEN, NUMBER: US/11/012,353

7 TITLE OF INVENTION: NUMBER: US/11/012,353

CURRENT APPLICATION NUMBER: FR 2004-12-16

6 PRIOR PILING DATE: 2003-12-16

6 PRIOR FILING DATE: 2003-01-20

6 PRIOR FILING DATE: 2003-01-20

6 PRIOR FILING DATE: 2003-01-20

6 PRIOR FILING DATE: 2002-05-07

6 PRIOR FILING DATE: 2002-05-07

6 PRIOR FILING DATE: 2002-05-07

7 PRIOR FILING DATE: 2002-01-18

8 PRIOR FILING DATE: 2002-01-18

9 PRIOR P
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62 PSLKORISITRDTSKNOPFLKINSVTTEDTATYYCAREGYGYFPDYWGGGTTLTVSS 118
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Publication No. US2005025532A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523P3

CURRENT APPLICATION NUMBER: US/11/054,515

CURRENT FILING DATE: 2005-02-10

PRIOR APPLICATION NUMBER: 60/543,296

PRIOR PLING DATE: 2004-02-11

PRIOR PLING DATE: 2004-06-18

PRIOR PLING DATE: 2004-06-18

PRIOR FILING DATE: 2004-1-14
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61 KPSLKDRITISRDTSKNOPSLKLSSVTAADTAVYYCARY-----GRVF-FDYWGQGTLV 113
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WS-11-054-515-1548

WS-11-054-515-1548

Sequence 1548, Application US/11054515

Publication NO. US2005025532A1

GENERAL INFORMATION:
APPLICATION WINDER: US/11/054,515

CURRENT APPLICATION WUMBER: US/11/054,515

CURRENT APPLICATION WUMBER: 60/543,296

PRIOR APPLICATION WUMBER: 60/580,347

PRIOR APPLICATION WUMBER: 60/580,347

PRIOR APPLICATION WUMBER: 60/303,418

PRIOR APPLICATION WUMBER: 60/303,418

PRIOR PILING DATE: 2001-11-14

PRIOR APPLICATION WUMBER: 60/31,469

PRIOR PILING DATE: 2001-11-16

PRIOR PILING DATE: 2001-11-16

PRIOR PILING DATE: 2001-12-19

PRIOR PILING DATE: 2001-12-19

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-17

PRI
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-12-19
PRIOR PILING DATE: 2001-16-15
PRIOR PLING DATE: 2001-66-15
PRIOR PLING DATE: 2001-66-15
PRIOR PLING DATE: 2001-06-25
PRIOR PLING DATE: 2001-06-25
PRIOR PLING DATE: 2001-03-21
PRIOR PLING DATE: 2001-03-21
PRIOR PLING DATE: 2001-03-16
PRIOR PLING DATE: 2001-03-16
PRIOR PLING DATE: 2001-03-16
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US-10-512-184-71
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    'S-10-512-184-71
    Sequence 71, Application US/10512184
    Sequence 71, Application US/10512184
    Publication No. US20050244901A1
    GENERAL INFORMATION: Gesellschaft zur F"rderung der angewandten Forschung e.V.
    TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
    TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
    TITLE OF INVENTION: resistance against fungi
    FILE REFERENCE: 3581.01US01
    CURRENT APPLICATION NUMBER: US/10/512,184

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TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: resistance against fungi
FILE REFERENCE: 3581.01US01
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 34
LENGTH: 259
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                                                                                                                                                                                                                                                                            62 PSLKDRITISRDTSKNQFSLKLSSVTAADTAVYYCAR----YGR-VFFDYWGQGTLVTVS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                     1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
                                                                                                                             Gaps
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                                                                                   Length 250;
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                                                                                                                           Indels
                                                                                 76.0%; Score 477.5; DB 7; 75.8%; Pred. No. 2.3e-35;
                                                                                                                           8; Mismatches
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Publication No. US20050244901A1
GENERAL INFORMATION:
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                                                                               Query Match
Best Local Similarity 75.8'
Matches 94; Conservative
                   ; ORGANISM: Homo sapiens
US-11-054-515-1548
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Best Local S
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: precursor OTHER INFORMATION: fusion protein comprising ACE - linker - OTHER INFORMATION: scrv PL2.
                                                                                                                                                                                                                                                                                                             2
                                                                                                                                                                                                                                                                    Length 371;
                                                                                                                                                                                                                                                                  ; Score 474.5; DB 6; Length
; Pred. No. 6.1e-35;
11; Mismatches 14; Indels
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CURRENT FILING DATE: 2004-10-22
NUMBER OF SEO ID NOS: 72
                                                                                                                                                                                                                                                                       75.6%;
                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                           91, Conservative
                     NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 71
LENGTH: 371
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 91; Conserv
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Run on:

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ORGANISM: Homo sapiens
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(cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/USIOA_PUBCOMB.pep:*

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                                         GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd
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US-10-735-916A-79
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US-10-735-916A-69
US-10-735-916A-26
US-10-383-447-24
US-10-383-447-24
US-10-383-447-24
US-10-383-477-26
US-10-383-677-28
US-10-383-677-28
US-10-399-762-125
US-10-309-762-127
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Maximum Match 100%
Listing first 45 summaries
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Result

Sequence Sequence

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70, Appl
37, Appl
20, Appl
20, Appl
21, Appl
114, Appl
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US-10-735-916A-75

Sequence 75, Application US/10735916A

Publication No. US2050084906A1

GENERAL INFORMATION:
APPLICANT: GOETSCH, Liliane
APPLICANT: GOETSCH, Liliane
APPLICANT: LEGER, Olivier
APPLICANT: DUFLOS, Alain
APPLICANT: BEEK, Alain
APPLICANT: BECK, Alain
APPLICANT: BOOT 12000
FILE REFERENCE: 017753-183
CURRENT FILING DATE: 2003-01-2-16
PRIOR APPLICATION NUMBER: FR 03/08 538
PRIOR FILING DATE: 2003-01-11
PRIOR PLING DATE: 2003-01-12
PRIOR FILING DATE: 2003-01-20

PRIOR FILING DATE: 2003-01-18

PRIOR FILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18
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Sequence 3
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Sequence
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ALIGNMENTS
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                               APPLICANT: CORVAIA, Nathalie
APPLICANT: LEGER, Olivier
APPLICANT: DUFLOS, Alain
APPLICANT: BECK, Alain
APPLICANT: HECW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: CORVAIA, Nathalie
APPLICANT: LEGER, Ollvier
APPLICANT: DUFLOS, Alain
APPLICANT: BECK, Alain
APPLICANT: HAEW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-183
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100.0%; Score 628; DB 5;
Best Local Similarity 100.0%; Pred. No. 5.1e-49;
Matches 117; Conservative 0; Mismatches 0;
                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT FILING DATE: 2003-12-16
PRIOR PAPLICATION NUMBER: EN 03/08 538
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-01-20
PRIOR PILING DATE: 2003-01-20
PRIOR APPLICATION NUMBER: FR 02/06
PRIOR APPLICATION NUMBER: FR 02/06
PRIOR APPLICATION NUMBER: FR 02/06
PRIOR PILING DATE: 2002-01-18
PRIOR SEQ ID NOS: 156
NUMBER OF SEQ ID NOS: 156
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APPLICANT: GOETSCH, Liliane APPLICANT: CORVAIA, Nathalie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-77
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ORGANISM: Homo sapiens
  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                      61 KPSLKDRVIISRDISKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVITVSS 117
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                                                                       Gaps
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JENDILGANT: GOETSCH, Liliane
JAPPLICANT: GOETSCH, Liliane
JAPPLICANT: GOETSCH, Liliane
JAPPLICANT: GOETSCH, Liliane
JAPPLICANT: LEGER, Ollvier
JAPPLICANT: DUFLOS, Alain
JAPPLICANT: BECK, Alain
JAPPLICANT: WAREN, Jean-Francois
JITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
JITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
JETLE PEPERBERE: 017753-183
CURRENT APPLICATION NUMBER: R03/08 538
PRIOR PILING DATE: 2003-01-10
PRIOR PILING DATE: 2003-01-20
PRIOR PILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 02/00 653
PRIOR APPLICATION NUMBER: FR 02/00 654
PRIOR APPLICATION NUMBER: FR 02/05 753
PRIOR APPLICATION NUMBER: PR 02/05 753
PRIOR APPLICATION NUMBER: PR 02/05 753
PRIOR APPLICATION NUMBER: PR 02/05 753
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Publication No. US20050084906A1
GENERAL INFORMATION:
APPLICANT: CORVAIA, Liliane
APPLICANT: CORVAIA, Nathalie
APPLICANT: LEGER, Olivier
APPLICANT: BUFLOS, Alain
APPLICANT: BUFLOS, Alain
APPLICANT: HECK, Alain
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      Length 117;
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                                                                    Indels
   Score 623; DB 5;
Pred. No. 1.2e-48;
                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 81, Application US/10735916A Publication No. US20050084906A1
   99.2%;
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SOFTWARE: PatentIn Ver. 2.1
                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-10-735-916A-81
Query Match
Best Local Similarity
Matches 115; Conserv
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19 QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLWNWIRQPPGKGLEWIGYISYDGTNNY 78
                                                                                       61 KPSLKDRITISRDTSKNOFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                     2 VQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNYK
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                                                                                                                                                                                                                                                                                                             Sequence 69, Application US/10735916A

Sequence 69, Application US/10735916A

Publication No. US20050084906A1

GENERAL INFORMATION:

APPLICANT: GOETSCH, Liliane

APPLICANT: GOETSCH, Liliane

APPLICANT: LEGER, Olivier

APPLICANT: DUFLOS, Alain

APPLICANT: HAEUW, Jean-Francois

TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF

FILE REFERENCE: 017753-183

CURRENT APPLICATION NUMBER: US/10/735,916A

CURRENT PILLING DATE: 2003-12-16

PRIOR FILING DATE: 2003-07-11

PRIOR FILING DATE: 2003-07-11

PRIOR FILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18

PRIOR PELING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18
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Sequence 52, Application US/10735916A

Publication No. US20050084906A1

GERREAL INFORMATION:

APPLICANT: CORVAIA, Nathalie

APPLICANT: CORVAIA, Nathalie

APPLICANT: BECR, Alain

APPLICANT: BECK, Alain

APPLICANT: BECK, Alain

APPLICANT: HAEUW, Jean-Francois

TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF

FILE REFERENCE: 017753-183

CURRENT FILING DATE: 2003-12-16

CURRENT FILING DATE: 2003-12-16

DELICATION NUMBER: US/10/735, 916A
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86.2%; Pred. No. 1.1e-41;
tive 8; Mismatches 8; Indels
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PRIOR APPLICATION NUMBER: FR 03/08 538
PRIOR FILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
PRIOR FILING DATE: 2003-01-20
PRIOR APPLICATION NUMBER: FR 02/00 653
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Best Local Similarity 86.29
Matches 100; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-735-916A-69
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APPLICANT: CORVER, Alain
APPLICANT: LEGER, Olivier
APPLICANT: LEGER, Olivier
APPLICANT: LEGER, Olivier
APPLICANT: BECK, Alain
APPLICANT: BECK, Alain
APPLICANT: HAEUW, Jean-Francois
TITLE BERERENCE: 017755-183
CURRENT FILIAG DATE: 2003-07-11
PRIOR PLLING DATE: 2003-07-11
PRIOR PLLING DATE: 2003-07-11
PRIOR PLLING DATE: 2003-07-11
PRIOR PLLING DATE: 2002-01-20
PRIOR PLLING DATE: 2002-01-18
PRIOR PLLING DATE: 2002-05-07
NUMBER OF SEQ ID NOS: 156
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FILE REFERENCE: 017753-183
CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT FILING DATE: 2003-12-16
PRIOR APPLICATION NUMBER: PR 03/08 538
PRIOR APPLICATION NUMBER: PR 03/08 538
PRIOR PILING DATE: 2003-01-20
PRIOR APPLICATION NUMBER: PR 02/00 653
PRIOR APPLICATION NUMBER: PR 02/00 654
PRIOR APPLICATION NUMBER: PR 02/00 654
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-05-07
PRIOR PILING DATE: 2002-05-07
PRIOR PILING DATE: 2002-05-07
PRIOR PILING DATE: 2002-05-07
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 83
LENGHALI 117
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APPLICANT: GOETSCH, Lillane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-10-735-916A-85
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US-10-735-916A-83
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US-10-735-916A-85
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LENGTH: 135
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Sequence 26. Application US/20040096392A1

Sequence 26. Application No. US20040096392A1

GENERAL INFORMATION:

APPLICANT: Bhaskar, Vinay

APPLICANT: Law, Debbie

APPLICANT: Ramakrishnan, Vanitha

APPLICANT: Ramakrishnan, Vanitha

APPLICANT: Afar, Daniel

APPLICANT: Nowers, David

FILE REFERENCE: 05882.0138.NPUS00

CURRENT APPLICATION NUMBER: US/0/383,447

CURRENT FILING DATE: 2002-03-08

PRIOR FILING DATE: 2002-03-08

PRIOR APPLICATION NUMBER: US 60/463,812

PRIOR FILING DATE: 2002-112-27

NUMBER OF SEQ ID NOS: 34

SOFTHAND 24

SOFTHAND 25

SOFTHAND 26
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                                                                                                                                                                                                                                                                                                                 Length 127;
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                                                                                                                                                                                                                                                                                                                 Query Match

86.9%; Score 546; DB 5;
Best Local Similarity 86.2%; Pred. No. 1.2e-41;
Matches 100; Conservative 8; Mismatches 8
               PRIOR APPLICATION NUMBER: FR 02/00 654
PRIOR FILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-05-07
PRIOR FILING DATE: 2002-05-07
PRIOR FILING DATE: 2002-05-07
SOFTWARE OF SEQ ID NOS: 156
SOFTWARE PARENTIN Ver. 2.1
SEQ ID NO 52
LENGTH: 127
TYPE: PRT
CREATION MEMBER DATE
TYPE: PRT
US-10-735-916A-52
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US-10-383-447-24
; Sequence 24, Application US/10383447
PRIOR FILING DATE: 2002-01-18
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LENGTH: 120
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APPLICANT: de la Calle, Agustin
APPLICANT: de la Calle, Agustin
APPLICANT: Carab, Ingrid
APPLICANT: Carab, Ingrid
APPLICANT: Carab, Ingrid
APPLICANT: Ramakrishnan, Vanitha
APPLICANT: Ramakrishnan, Vanitha
APPLICANT: Murray, Richard
APPLICANT: Murray, Richard
APPLICANT: Murray, Richard
APPLICANT: Powers, David
ITILE OF INVENTION: Antibodies Against Cancer Antigen TWEFF2 and Uses Thereof
FILE REFERENCE: 05882.0138 NPUS00
CURRENT APPLICATION NUMBER: US 60/362,837
PRIOR PILING DATE: 2002-03-08
PRIOR PLING DATE: 2002-03-08
PRIOR PLING DATE: 2002-12-27
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.2
SEQ ID NO 28
LENGTH: 120
LENGTH: 120
LENGTH: 120
                                                                                                                                          APPLICANT: Caras, Ingrid
APPLICANT: Caras, Ingrid
APPLICANT: Ramakrishnan, Vanitha
APPLICANT: Ramakrishnan, Vanitha
APPLICANT: Ramakrishnan, Vanitha
APPLICANT: Remakrishnan, Vanithard
APPLICANT: Powers, David
APPLICANT: Powers, David
TITLE OF INVENTION: Antibodies Against Cancer Antigen TMEFF2 and Uses Thereof
FILE REPERENCE: 05882.0138 MPUS00
CURRENT APPLICATION NUMBER: US/10/383,447
CURRENT FILING DATE: 2002-03-08
PRIOR PILING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: US 60/463,812
PRIOR PILING DATE: 2002-12-27
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.2
SEG ID NO 24
LENGTH: 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 28, Application US/10383447; Publication No. US20040096392A1; GENERAL INFORMATION:
APPLICANT: Bhaskar, Vinay
APPLICANT: de la Calle, Agustin; APPLICANT: Law, Debbie
                                                APPLICANT: Bhaskar, Vinay
APPLICANT: de la Calle, Agustin
US20040096392A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-383-447-24
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us-10-735-916a-75.rapbm

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Query Match
Best Local Similarity
Matches 98; Conserv
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                                                                        2 VOLOBSGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNYK 61
                                                                                                 2 VQLQESGPGLVKPSETLSLTCAVSGYSITSGYYWSWIRQPPGKKLEMMGFISYDGSNKYN 61
                                                                                                                                                                                                 62 PSLKNRITISRDTSKNQFSLKLSSVTAADTATYYCARGLRRGDYSMDYWGQGTLVTVSS 120
                                                                                                                                                                    62 PSLKDRITISRDTSKNQFSLKLSSVTAADTAVYYCA---RYGRVFFDYWGQGTLVTVSS 117
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APPLICANT: Glads, Jean
APPLICANT: FOLTS, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
FILE REPERCECE ABGENIX. 1027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR APPLICATION NUMBER: 60/337275
PRIOR APPLICATION NUMBER: 60/337275
SOFTWARE: FastSEQ for Windows Version 4.0
SSOTWARE: FastSEQ for Windows Version 4.0
ILENGTH: 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 119;
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                            13; Indels
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80.1%; Score 503; DB 4;
Best Local Similarity 81.7%; Pred. No. 8.7e-38;
Matches 98; Conservative 7; Mismatches 11;
  83.2%; Pred. No. 2.8e-38;
tive 4; Mismatches 13
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BEDIAN, VAHE
APPLICANT: GLADUE, RONALD P.
APPLICANT: OCNVALAN, JOSE
APPLICANT: OCNVALAN, JOSE
APPLICANT: OCNVALAN, JOSE
APPLICANT: JIA, XIAO-CHI
APPLICANT: FENG, XIAO-CHI
TITLE OF INVENTION: ANTIBODIES TO CD40
ITILE REFERENCE: ABX-PF/3 US
CURRENT APPLICATION NUMBER: US/10/292,088
CURRENT FILING DATE: 2003-03-14
FRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PATENTING DATE: 201-11-09
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PATENTING DATE: 201-11-09
                                                                                                                                                                                                                                                                                                                                              Sequence 143, Application US/10309762 Publication No. US20040018198A1 GENERAL INFORMATION:
                         99; Conservative
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US-10-309-762-143
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US-10-292-088-109
     Best Local Similarity
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US-10-292-088-109
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US-10-309-762-143
                            Matches
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APPLICANT: Deligher Colling of the C
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                                                                                                                                                                                      1 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYMSWIRQPPGKGLEWIGYIXYSGSTNY
                                                                                                                                                   1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
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   DB 4; Length 118;
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                                                                         12; Indels
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79.7%; Score 500.5; DB 4.
larity 82.4%; Pred. No. 1.5e-37;
Conservative 6; Mismatches 12.
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Pred. No. 1.8e-37;
6; Mismatches 13
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 56
LENOTH: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 56, Application US/10805177
Publication No. US20050084449A1
GENERAL INFORMATION:
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81.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98; Conservative
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Best Local Similarity
Matches 98; Conserv
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7
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79.5%; Score 499.5; DB 4; Length 122;
Best Local Similarity 80.5%; Pred. No. 1.9e-37;
Matches 99; Conservative 5; Mismatches 12; Indels 7; Gaps
; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 25; LEWOTH: 122; TYPE: PRT: 7 ORGANISM: Homo sapiens US-10-309-762-25
                                                                                                                                                                                                                                                                                  Search completed: January 10, 2006, 21:35:32 Job time : 64.1754 secs
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| 120 VSS 122
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Sequence 6, Sequence 7, Sequence 7, Sequence 9, Sequence 5, Sequen

Sequence 837, Sequence 3, Ag Sequence 2, Ag

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79.0%; Score 496; DB 2; Length 119; 81.7%; Pred. No. 4.8e-42; ive 6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New York

CUNTRY: USA

ZIP: New York

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Pacentine

MEDIUM TYPE: Poss/MS-DOS

SOFTWARE: Pacentine

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Pacentine

SOFTWARE: Pacentine

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Pacentine

SOFTWARE: Pacentine

OPERATING DATE: US/09/025,769B

FILING DATE: 18-F8E-1998

FILING DATE: 18-ANG-1995

ATTORNEY/AGENT NUMBER: EP 95 11 3021.0

FRIGNATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELEFRONE: (212)596-9090

TELEFRAX: (212)596-9090

SOFTWARE: CARRACTERISTICS:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B: James F. Haley, Jr., Esq. c/o Fish & Neave 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Knappik, Achim
APPLICANT: Rappik, Achim
APPLICANT: Pack, Peter
APPLICANT: 11ag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
CORRESPONDENCE ADDRESS:
US-09-343-698-6

US-08-325-955-6

US-09-273-453-7

US-09-273-453-7

US-10-330-613A-9

US-08-360-125-5

US-08-450-578-5

US-09-017-628-5

US-09-017-628-5

US-09-017-628-5

US-09-017-628-5

US-09-017-628-5

US-09-125-539-5

US-08-55-5

US-08-55-5

US-08-77-128-18

US-08-77-128-18

US-08-77-128-18

US-08-77-128-18

US-08-77-128-18

US-08-767-128-18

US-08-76-128-18
                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                       Sequence 39, Application US/09025769B Patent No. 6300064
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 119 amino acids
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  TOPOLOGY: linear
MOLECULE TYPE: protein
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Best Local Similarity
Matches 98; Conserv
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                                                                                                                                                                                                                                                                                                                             US-09-025-769B-39
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468.5
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    65, Appl
39, Appl
39, Appl
65, Appl
2, Appli
113, Appli
4, Appli
64, Appli
64, Appli
69, Appli
                                                                                        January 10, 2006, 20:34:27; Search time 22.847 Seconds (without alignments) 423.384 Million cell updates/sec
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Sequence 39,
Sequence 65,
Sequence 39,
Sequence 65,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 39,
                                                                                                                                                                         1 QVQLQESGPGLVKPSETLSL......RYGRVFFDYWGQGTLVTVSS 117
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'/ Ggn2 6/ptodata1/jaa/5_COMB.pep:*

' / Ggn2 6/ptodata1/jaa/6_COMB.pep:*

' / Ggn2 6/ptodata1/jaa/H_COMB.pep:*

' / Ggn2 6/ptodata1/jaa/H_COMB.pep:*

' / Ggn2 6/ptodata1/jaa/PCTUS_COMB.pep:*

' / Ggn2 6/ptodata1/jaa/RE_COMB.pep:*

' / Ggn2 6/ptodata1/jaa/Re_COMB.pep:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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US-09-490-153-65

US-09-490-153-65

US-09-490-324-39

US-09-490-324-39

US-09-490-324-39

US-09-09-09-139-13

US-09-09-09-139-13

US-08-137-1170-69

US-08-137-1170-69

US-08-137-1170-69

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US-10-330-613A-17
US-09-800-729-145
US-10-330-613A-5
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                                                                                                                                                                                                                                             572060 seqs, 82675679 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                    OM protein - protein search, using sw model
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628
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seq length: 200000000
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Match Length
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479.5
478.5
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471
470.5
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 NPSLKSRVTISVDTSKNQPSLKLSSVTAADTAVYYCARWGGDGFYAMDYWGQGTLVTVSS 119
                                                                                        61 KPSLKDRITISRDTSKNOFSLKLSSVTAADTAVYYCARYGRVFF---DYWGQGTLVTVSS 117
                                                                                                               1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY 60
9
                          QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGYIYYSGSTNY 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGYIYYSGSTNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCLES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION NUMBER: 27,794
PRICRATION NUMBER: 27,794
PRILING DATE: 11-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REFERENCE/DOCKET NUMBER: 27,794
REFERENCE/DOCKET NUMBER: 27,794
REFERENCE/DOCKET NUMBER: 27,794
REFERENCE/COMPUTION INFORMATION:
TELEPHONE: (212)596-9000
TELEPHONE: (212)596-9000
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.0%; Score 496; DB 2; Length 119; 81.7%; Pred. No. 4.8e-42; ive 6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                           APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ge, Liming
APPLICANT: Ge, Liming
APPLICANT: Ge, Liming
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Procein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
                                                                                                                                                                                                                                                Sequence 65, Application US/09025769B Patent No. 6300064
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 81.7
Matches 98; Conservative
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Sequence 39, Application US/09490070A Patent No. 6696248

US-09-490-070A-39

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61 KPSLKDRITISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFF---DYWGQGTLVTVSS 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 OVOLOESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                             Ge, Lining
Moroney, Simon
Plueckthun, Andreas
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
Milte & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 65, Application US/09490070A
; Sequence 65, Application US/09490070A
; Patent No. 6596248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Knappik, Achim
; Ge, Liming
; Ge, Liming
; Moroney, Simon
Plueckchun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES:
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INPORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REPERBUCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPAX: (202) 912-2000
TELEPAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 496; DB 2;
Pred. No. 4.8e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 79.0%; Score 496; DB Best Local Similarity 81.7%; Pred. No. 4.8e-Matches 98; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-490-070A-39
                                                                                                                                                                                                                                                                                                                                                                ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: <Unknown>
APPLICANT: Knappik, Achim
                                                                                                                                                                                                                                                                                               CITY: Washington STATE: D.C.
                                                Ilag,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-490-070A-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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CITY: New York
STATE: New York
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US-09-490-153-65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 KPSLKDRITISRDTSKNOFSLKLSSVTAADTAVYYCARYGRVFF---DYWGQGTLVTVSS 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Gaps
                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: COlin G. Sandercock, ESG.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 31,298
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G. Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James P. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 79.0%; Score 496; DB 2; Length 119; Best Local Similarity 81.7%; Pred. No. 4.8e-42; Matches 98; Conservative 6; Mismatches 12; Indels
White & McAuliffe
6 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 39, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 65:
                                                    CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-490-070A-65
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60 NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARWGGDGFYAMDYWGQGTLVTVSS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4
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Patent No. 6706484

GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Back, Peter
Ilag, Vic
Ge, Liming
MOTONEY, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESSE:
ADDRESSE: James F. Haley, Jr., Esq. c/o Fish & Ne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 79.0%; Score 496; DB 2; Length 119; Best Local Similarity 81.7%; Pred. No. 4.8e-42; Matches 98; Conservative 6; Mismatches 12; Indels
                PRIOR ALLICATION DATA:

APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-FG9-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEPHONE: (212)596-9090
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794 REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECTLE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
FILING DATE: 24-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10021
COMPUTER READABLE FORM:
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Ilag,
                                       Query Match
Best Local Similarity
Matches 98; Conserv
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  US-09-490-324-39
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                                                                                                                                                                                                                                                                                                                                                                                                                             29
                                                                                                                                                                                                                                                                                                                        1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY 60
                                                                                                                                                                                                                                                                                                                                            1 QVQLQBSGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGYIYYSGSTNY
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                  4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York STATE: New York
                                                                                                                                                                                                                                           Length 119;
                                                                                                                                                                                                                                                                                12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
                                                                                                                                                                                                                                         79.0%; Score 496; DB 2;
81.7%; Pred. No. 4.8e-42;
tive 6; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: 27,794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAT: (212)596-9000
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                   TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-490-153-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
                TELEPHONE: (212)596-9000
TELEFAX: (212)596-9000
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acids
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 39, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                     Query Match 79.0°
Best Local Similarity 81.7
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-490-324-39
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61 KPSLKORITISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFF---DYWGQGTLVTVSS 117
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                                                                                                                1 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGYIYYSGSTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGYIXYSGSTNY
                                                                                       1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDUW TYPE: Ploppy disk

COMPUTER: IBM PC compatible

CORRATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,324

FILING DATE: 24-Jan-2000

PRIOR APPLICATION NUMBER: US/09/025,769

FILING DATE: 18-FEB-199

FILING DATE: 18-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 496; DB 2; Length 119;
Pred. No. 4.8e-42;
6; Mismatches 12; Indels
  Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tagy, vir.
Ge, Liming
Moroney, Simon
Plueckthuu, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
Score 496; DB 2;
Pred. No. 4.8e-42;
6; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear;
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-490-324-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                 Sequence 65, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
79.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 81.7%;
Matches 98; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: New York
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61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGD-GFDYWGQGTLVTVSS 117

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60 YKPSLKDRITISRDTSKNOPSLKLSSVTAADTAVYYCAR------YGRVFFDYWGQG 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 QVQLQESGPGLVKPSETLSLTCAVSGGSITSGGYYWSWIRQPPGKGLEWIGYIYYSGSTL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 473;
                                                                                                                                                                                                                         APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.8%; Score 482.5; DB 2; 77.2%; Pred. No. 5.6e-40; tive 4; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: 10 Basette COMPUTER: DISSECTE COMPUTER: DISSECTE COMPUTER: DISSECTE COMPUTER: DISSECTE CORRESING SOFTWARE: FASES FOR WINDOWS VERSION 2.0 CURRENT APPLICATION NUMBER: US/09/049,672A FILING DATE: HEREWITH CLASSIFCATION NUMBER: US/09/049,672A APPLICATION NUMBER: BFLIAM APPLICATION NUMBER: ATTORNEY/AGENT INFORMATION: NAME: CETTON, MICHAEL CRECOMMUNICATION INFORMATION: REGISTRATION NUMBER: BF-0497 US REGISTRATION INFORMATION: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                                                                                              ; Sequence 4, Application US/09049672A; Patent No. 6135941
                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 473 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIBRARY: PANCTUT01
CLONE: 1513264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 3174 Port
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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1 QVQLQESGPGLVKPSETLSLTCTVSGYSI-TGGYLWNWIRQPPGKGLEWMGYISYDGTNN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWTWIRQHPGKGLEWIGFIYYSGSTY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYMGWIRQPPGKGLEWIGSIYHSGSTYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 YKPSLKDRITISRDISKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 KPSLKDRITISRDISKNOPSLKLSSVIDADIAVYYCARYGRVPFDYWGQGILVIVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 76.9%; Score 483; DB 2; Length 117; Best Local Similarity 81.4%; Pred. No. 9.3e-41; Matches 96; Conservative 6; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13, Application US/10330613A

Patent No. 6924360

GENERAL INFORMATION:

APPLICANT: Gudas, Jean

TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
FILE REFERENCE: ABGENIX.022A

CURRENT APPLICATION NUMBER: 05/24

CURRENT PILING DATE: 2002-12-26

PRIOR PILING DATE: 2001-12-18

PRIOR FILING DATE: 2001-12-18

NUMBER OF SEQ 1D NOS: 90

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Tempest, Philip R
APPLICANT: Tempest, Philip R
APPLICANT: Tempest, Philip R
APPLICANT: Holet, Thor L
APPLICANT: Ackson, Helen
APPLICANT: Jackson, Helen
APPLICANT: Jackson, Helen
APPLICANT: Jackson, Relen
APPLICANT: Jackson, Relen
APPLICANT: Jackson, Nelen
APPLICANT: BABACP575333
CURRENT APPLICATION NUMBER: US/09/720,493
CURRENT FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: GB 9814383.7
                                                                                                                                        Sequence 2, Application US/09720493
Patent No. 6827925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo Sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-330-613A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 2
LENGTH: 117
TYPE: PRT
                                                                                             RESULT 9
US-09-720-493-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-720-493-2
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US-08-436-717-64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 KPSLKDRITISRDTSKNQFSLKLSSVTAADTAVYYÇAR--YGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Gaps
Sequence 64, Application US/08137117D

Sequence 64, Application US/08137117D

Patent No. 579585

GENERAL INFORMATION:

APPLICANT: TSUCHIYA, Masayuki
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: JONES, Steven

APPLICANT: JONES, Steven

TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN

TITLE OF INVENTION: INTERLEUKIN'6 RECEPTOR

NUMBER OF SEQUENCES: 158

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

CONDITES: Patent N.W., Suite 500

CITY: Washington

STATE: D.C.

CONDITES: READABLE PORM:

MEDIUM TYPE: Plopy disk

COMPUTER: Patent N. Release #1.0, Version #1.30

COMPUTES: 20-055/MS-DOS

SOFTWARE: Patent N. Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: WO PCT/JP92/00544

FILING DATE: 2-A-ARP.1991

PRIOR APPLICATION NUMBER: MAP.1992

RIGH APPLICATION NUMBER: B. 25-288

FILING DATE: 2-A-ARP.1991

ATTORNEY/AGENT INFORMATION:

NAME: WEGNEY, HAROLD C.

RECETRALION NUMBER: 53-288

FILING DATE: 2-A-ARP.1991

ATTORNEY/AGENT INFORMATION:

NAME: WEGNEY, HAROLD C.

TELEPHONE: (202)672-5399

TELEPHONE: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 76.8%; Score 482; DB 1; Length 123; Best Local Similarity 75.6%; Pred. No. 1.2e-40; Matches 90; Conservative 11; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 904136
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-137-117D-64
             US-08-137-117D-64
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Sequence 64, Application US/08436717 Patent No. 5817790 GENERAL INFORMATION: APPLICANT: TSUCHIYA, Masayuki

RESULT 13 US-08-436-717-64

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61 KPSLKDRITISRDISKNQPSLKLSSVTAADIAVYYCAR--YGRVPFDYWGQGTLVTVSS 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.8%; Score 482; DB 1; Length 123; 75.6%; Pred. No. 1.2e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16; Indels
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, JOSE
TITLE OF INVENTION: RESHARED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR:1992
PRIOR APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 19-FEB-1992
PRIOR APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REGISTRATION NUMBER: 25,258
REGISTRATION NUMBER: 25,258
TELERRENCE/DOCKET NUMBER: 25,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Mismatches
                                                                                                                                  STREET: 3000 K Street, N.W., Suite 500 CITY: Washington STATE: D.C. COUNTRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 69, Application US/08137117D
Patent No. 5795965
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, JOSE
                                                                                                                                                                                                                                                                                                                            ZIP: 20007-5109
COMPUTER READABLE FORM:
CMPUTER TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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US-08-137-117D-69
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STATE: D.C.
COUNTRY: USA
ZIP. 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPES: PLOAPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 138 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-08-436-717-69
              Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY 60
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TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN NUMBER OF SEQUENCES:

NUMBER OF SEQUENCES:
SCORRESPONDENCES:
ADDRESSEE: FOLEY & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STREET: 1000
COUNTRY: USA
ZIP: 20007-5109
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFPCATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
RRIOR APPLICATION NUMBER: US/08/137,117D
RIUNG DATE: 24-APR-1992
RRIOR APPLICATION NUMBER: US/08/176
FILING DATE: 25-APR-1991
ATTORNEY AGENT INFORMATION:
NAME: WEGGENER, HATOR OF THE STANCE APPLICATION NUMBER: 25,258
REPERENCE/DOCKET NUMBER: 25,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TO HUMAN
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Sequence 69, Application US/08436717
Sequence 69, Application US/08436717
Sequence 69, Application US/08436717
APPLICANT: SATO, Koh
APPLICANT: SATO, Koh
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
TITLE OF INVENTION: ADDRESSE:
CORRESPONDENCE ADDRESSE:
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 138 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: protein US-08-137-117D-69
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20 QVQLQESGPGLVRPSQTLSLTCTVSGYSITSDHAMSWVRQPPGRGLEWIGYISYSGITTY 79
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OPERATING SYSTEM:
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
FILING DATE: US/08/436,717
FILING DATE: US/08/137,117
APPLICATION NUMBER: US/08/137,117
FILING DATE: 24-APR-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/126/AAOK
FILING DATE: 15-FEB-1992
ATORNEY/AGENT INFORMATION:
NAME: WEGNER, HAROID C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET UNBER: 53466/126/AAOK
TELEPHONE: (202)672-5309
TELEFFX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: January 10, 2006, 20:58:04 Job time : 22.847 secs
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RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                            ADJ76909
                                                                                   January 10, 2006, 20:07:41; Search time 80.7649 Seconds (without alignments) 636.505 Million cell updates/sec
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1 QVQLQESGPGLVKPSETLSL......RYGRVFFDYWGQGTLVTVSS 117
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version 5.1.6
- 2006 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                            protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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geneseqp2001s:*
geneseqp2003s:*
geneseqp2003as:*
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geneseqp1990s:*
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seq length: 200000000
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                                                                                                                                                                                                                                                                                                                     Minimum DB
Maximum DB
                                                            OM protein
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                                                                                                                                                                                  Sequence:
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                                                                                          Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Adj76909 Anti-IGF-	Adz67079 Human ant	Adj76911 Anti-IGF-	Adz67081 Human ant	Adj76913 Anti-IGF-		Adj76915 Anti-IGF-		Adj76917 Anti-IGF-		Adj76919 Anti-IGF-		Adj76903 Anti-IGF-		Adj76886 Anti-IGF-	Adz67056 Murine im	Adc27457 Humanised	Adc27455 Humanised	Adc27459 Humanised	9	Adp03973 Murine-ex	Ads16559 Human ant	Adp03885 Murine-ex	Adp03889 Murine-ex
SUMMARIES	ΙD	ADJ76909	ADZ67079	ADJ76911	ADZ67081	ADJ76913	ADZ67083	ADJ76915	ADZ67085	ADJ76917	ADZ67087	ADJ76919	ADZ67089	ADJ76903	ADZ67073	ADJ76886	ADZ67056	ADC27457	ADC27455	ADC27459	AAY15126	ADP03973	ADS16559	ADP03885	ADP03889
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ouerv	Match	0.0	100.0	100.0	100.0	99.5	99.5	99.5	99.5	97.3	97.3	97.3	97.3	86.9	86.9	86.9	86.9	84.6	81.4	81.0	80.5	80.1	80.0	79.5	79.5
	Score	628	628	628	628	623	623	623	623	611	611	611	611	546	546	546	546	531.5	511.5	508.5	505.5	503	502.5	499.5	499.5
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Adp03958 Murine-ex	_	Abb07171 ebvHigM M	Adi26658 Human ant	Adp03887 Murine-ex	Adp03884 Murine-ex	Aaw27554 Human Ab	Abj18676 Antibody	Ade28455 Human ant	Ade28479 Human ant	Ady74798 Human 1gG	Aec20804 Low+ mode	Aec20877 Low + mod	Aay44615 Human ant	Ade28491 Human ant	Ade28471 Human ant	Aao30915 dI-NHS76	Aao30913 dI-NHS76	Aea21456 Human ant	Adx98267 Human ant	Ads16505 Human ant	
ADP03958	ADP03957	ABB07171	ADI26658	ADP03887	ADP03884	AAW27554	ABJ18676	ADE28455	ADE28479	ADY74798	AEC20804	AEC20877	AAY44615	ADE28491	ADB28471	AA030915	AA030913	AEA21456	ADX98267	ADS16505	
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120	116	121	121	122	122	119	119	121	466	119	118	467	117	121	466	280	280	122	139	121	
79.4	79.1	79.1	79.1	79.1	79.1	79.0	79.0	79.0	79.0	78.7	78.6	78.6	78.5	78.5	78.5	78.5	78.5	78.3	78.3	78.1	
498.5	496.5	496.5	496.5	496.5	496.5	496	496	496	496	494	493.5	493.5	493	493	493	493	493	491.5	491.5	490.5	
25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region; CDR. (FABR ) FABRE MEDICAMENT SA PIERRE. ADJ76909 standard; protein; 117 AA Anti-IGF-1R related protein #22. Leger O; 18-JAN-2002; 2002FR-0000653. 18-JAN-2002; 2002FR-0000654. 07-MAY-2002; 2002FR-0005753. 20-JAN-2003; 2003WO-FR000178. 06-MAY-2004 (first entry) Goetsch L, Corvaia N, WPI; 2003-569653/53. WO2003059951-A2 Homo sapiens. 24-JUL-2003. ADJ76909; 

New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.

Disclosure; SEQ ID NO 75; 164pp; French.

The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-18) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or-2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-1R. Ab and its fragments are used to prevent or rear diseases associated with overexpression and/or abnormal activity of IGF-1R and/or epidermal growth factor receptor (BGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of

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          transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the proliferation of tumor cells, so are useful against cancers of the abootstate, bung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; heavy chain variable region.
                                                                                                                                                                                                      9
                                                                                                                                                                                                                       QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
                                                                                                                                                                                                                                                              KPSLKDRITISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                              QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human antibody 7C10 1 heavy chain variable region SEQ ID NO:75.
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                                                                                                                                              Length 117;
Especially they inhibit
                                                                                    protein sequence used to generate the Ab of the invention
                                                                                                                                                                        Indels
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                                                                                                                                             Score 628; DB 7;
Pred. No. 3.2e-49;
0; Mismatches 0;
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receptors with their ligands.
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                                                                                                                                             100.0%;
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20-JAN-2003; 2003WO-FR000178.
11-JUL-2003; 2003FR-00008538.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                         Matches 117; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2005-321968/33
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CORVAIA N.
LEGER O.
                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DUFLOS A. HAEUW J.
                                                                                                                 Sequence 117 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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The invention relates to a novel isolated anti-inalin-like growin ractor of receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of epable of binding to human IGF-IR and, if necessary, capable of appetifically inhibiting tyrosine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary of determining region (CDR) consisting of one of two fully defined is amino acids (ADZ67006 and ADZ67014). An antibody of the prevention or treatment of an edicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or Connected with a cutivation of the IGF-IR and/or EGFR, and/or connected with a cutivation of the IGF-IR and/or EGFR, and/or connected with inhibition of the insulin render interaction of IGF1 or IGF2 with IGF-IR and/or EGF with EGFR where the administration of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral caparation of a medicament intended to inhibit the growth and/or IGF2-dependent and/or IGF2-dependent and/or IGF2-dependent cells, I) is useful in the preparation of a medicament intended for prevention or of the transformation or intended for prevention or for the treatment of psoriads. (I) is useful in preparation of a medicament intended for prevention or for the treatment of psoriads. (I) is useful in preparation of a medicament intended for prevention or colls prevention or a medicament intended for prevention or colls prevention of a medicament intended for the prevention of a medicament intended for the prevention of a medicament intended for the prevention of a medicament intended for prevention of a medicament intended for the prevention of a medicament intended for the prevention of a medicament
The invention relates to a novel isolated anti-insulin-like growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KPSLKDRITISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYLSYDGTNNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 628; DB 9;
100.0%; Pred. No. 3.2e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytostatic, antipsoriatic; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-IGF-1R related protein #23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADJ76911 standard; protein; 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003059951-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 117 AA;
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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of normal cells, so are useful against cancers of the proliferation of tumor cells, so are useful against cancers of the prostate. Iung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein sequence used to generate the Ab of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, SEQ ID NO 77; 164pp; French
                                                                                                                                                                                                                                                                                                    (FABR ) FABRE MEDICAMENT SA PIERRE.
20-JAN-2003; 2003WO-FR000178.
                                                                                               18-JAN-2002; 2002FR-00000653.
18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
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                                                                                     QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
                                                                1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
                                 Gaps
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 Length 135;
                                 Indels
100.0%; Score 628; DB 7;
100.0%; Pred. No. 3.8e-49;
tive 0; Mismatches 0;
              Best Local Similarity 100.
Matches 117; Conservative
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    Query Match
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Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; heavy chain variable region.
                                                                                                      Human antibody 7C10 1 heavy chain variable region SEQ ID NO:77.
                                                                                                                                                                                                                                                                                                          /note= "leader peptide"
49. .54
                                                                                                                                                                                                                                                                                              Location/Qualifiers
              ADZ67081 standard; protein; 135 AA
                                                                         (first entry)
                                                                                                                                                                                                                                                               Homo sapiens
                                                                           30-JUN-2005
                                                                                                                                                                                                                                                                                                          Peptide
ADZ67081
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Sequence 135 AA;

49. .54 /note= "CDR1"

Region

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The invention relates to a novel isolated anti-insulin-like growth factor

I receptor (IGF-IR) antibody (I) or its functional fragment, being
capable of binding to human IGF-IR and, if necessary, capable of
specifically inhibiting tyrosine kinase activity of the receptor,
comprising a light or heavy chain having at least one complementary
determining region (CRR) consisting at least one complementary
caids (ADZ67006 and ADZ67014). An antibody of the invention is useful in
the preparation of a medicament intended for the prevention or treatment
of an illness connected with an overexpression and/or an abnormal
activation of the IGF-IR and/or EGFR, and/or of EGFR, and box of EGFR, and/or EGFR, and and/or EGFR, and and and/or EGFR, and/or EGFR, and/or EGFR, and/or EGFR, and and and and and and and and and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (I), which is optionally labeled. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beck A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Duflos A, Haeuw J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 13; SEQ ID NO 77; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leger O,
                   "CDR2"
                                                          /note= "CDR3"
                                                                                                                                                                                                                                             18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-00005753.
07-JAN-2003; 2003WO-FR000178.
11-JUL-2003; 2003FR-00008538.
                                                                                                                                                                                   16-DEC-2003; 2003US-00735916
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                                         . .124
69. .84
/note= "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2005-321968/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for treating
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CORVAIA N.
LEGER O.
                                                                                                                                                                                                                                                                                                                                                                                                             DUFLOS A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ADZ67080
                                                                                                     US2005084906-A1
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                                                                                                                                            21-APR-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                   (DUFL/)
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Gaps

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Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-1R and/or BGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         insulin-like growth factor-1 receptor; IGP-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                            KPSLKDRITISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                              KPSLKDRITISRDISKNOFSLKLSSVTAADTAVYYCARYGRVFFDYWGGGTLVIVSS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                           OVOLOESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIROPPGKGLEWMGYISYDGTNNY
                                                                                       QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
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                    Length 135;
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                                                    Indels
                  Score 628; DB 9;
Pred. No. 3.8e-49;
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Pred. No. 9.2e-49;
100.0%; Sco...
100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic; antipsoriatic; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (FABR ) FABRE MEDICAMENT SA PIERRE
                                                                                                                                                                                                                                                                                      ADJ76913 standard, protein, 117 AA
                                                                                                                                                                                                                                                                                                                                                                                          Anti-IGF-1R related protein #24.
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18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
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                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                  Local Similarity 100.
Les 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goetsch L, Corvaia N,
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Best Local Similarity
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Matches
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The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tronine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal hyperactivation of the IGF-IR and/or connected with a hyperactivation of the IGF-IR and/or connected with a interaction of the EGFR, and or EGFR, and/or of EGF with EGFR, where
                                                                                                                                                                                                                                                                                              Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipeoriatic; psoriasis; dermatological disease; immune disorder; heavy chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
                                                           1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWIGYISYDGTNNY
QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
                                                                                                                                                                                                                                                                      Human antibody 7C10 2 heavy chain variable region SEQ ID NO:79.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beck A;
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2002FR-00005753.
2003WO-FR000178.
2003FR-00008538.
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CORVAIA N.
LEGER O.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2005084906-A1.
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the administration of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin creeptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral character, preferably IGF-dependent, especially IGF1 and/or IGF2- cdependent and/or EREX/neu-dependent cells. (I) is useful for preparation of a medicament intended to inhibit the growth and/or the proliferation of tumor cells, preferably IGF-dependent, and/or the proliferation of tumor cells, preferably IGF-dependent, cells. (I) is useful in the preparation of a medicament intended for prevention or for the treatment of cancer, breast cancer, endometrial cancer of colon cancer. (I) is useful in the preparation of a medicament intended for the prevention or for the preparation of a medicament intended for the prevention or for the treatment of psoriais. (I) is useful in preparation of a medicament colon cancer. (I) is useful in the prevention or for the treatment of psoriais. (I) is useful in preparation of a medicament colon cancer is comparation or an underexpressing of a biologically active compound to cells expressing or overexpressing of the IGF-IR and/or EGFR receptor is useful for in vitro diagnosis of illnesses induced by an coverexpression of the IGF-IR and/or EGFR receptor is suspected, which involves contacting the convertion of a medicament in which the abnormal present convertion of the invention of the in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 623; DB 9; Length 117;
Pred. No. 9.2e-49;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic; antipsoriatic; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (FABR ) FABRE MEDICAMENT SA PIERRE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-IGF-1R related protein #25.
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07-MAY-2002; 2002FR-00005753.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.24;
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Best Local Similarity 98.3
Matches 115; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 117 AA;
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WPI; 2003-569653/53

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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or creat diseases associated with overexpression and/or abnormal activity of IGF-IR. Ab and its fragments are used to prevent or IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; heavy chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 KPSLKDRITISRDTSKNQPSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
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                                                                                                                                                                                                                                                                                                                                                                                                                               Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 623; DB 7; Length 13
Pred. No. 1.1e-48;
2; Mismatches 0; Indels
                                                      Disclosure, SEQ ID NO 81; 164pp; French
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/note= "leader peptide"
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.= "CDR1"
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/note= "CDR2"
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/note= "CDR3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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Matches 115; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                            Sequence 135 AA;
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insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;

cytostatic; antipsoriatic; antibody;

Anti-IGF-1R related protein #26.

06-MAY-2004 (first entry)

ADJ76917;

ADJ76917 standard; protein; 117 AA.

RESULT 9 ADJ76917

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The invention relates to a novel isolated anti-insulin-like growth factor capable of binding to human IGF-IR and, if necessary, capable of capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tynoshie kinase activity of the receptor, capable of specifically inhibiting tynoshie kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining a region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in a cids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended of an illness connected with an overexpression and/or a bnormal colf an illness connected with IGF-IR and/or CG far illy defined by the interaction of the Irransduction pathway of the signal mediated by the interaction of the transduction pathway of the signal mediated by the interaction of the receptor. The antibody is useful for preparation of a medicament intended to interaction of transformation of normal cells into cells with tumoral capacity in the preferably IGF-dependent, especially IGF1 and/or IGR2-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent cells, in the preparation of a medicament intended for prevention or too the treatment of cancer, where the cancer is chosen from prostate cancer. Osteosarcom, lung cancer, capacitally IGF1-and/or IGF2-dependent and/or EGF dependent cells. (I) is useful in the preparation of a medicament intended for prevention or col the presention of a medicament intended for prevention or col con cancer. (I) is useful in the preparation of a medicament intended for the present cancer, endometrial cancer or colon cancer. (I) is useful in the preparation of a medicament intended for the specific targeting of the IGF-IR and/or EGFR receptor. (I) is useful for in vitro diagnosis of illnesses induced con the present of intended for the specific targ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                            Beck A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 135;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Duflos A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 13; SEQ ID NO 81; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                            Leger O,
2002FR-00005753.
2003WO-FR000178.
                                                                        11-JUL-2003; 2003FR-00008538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful for treating cancer.
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                                                                                                                                                    GOETSCH L.
CORVAIA N.
LEGER O.
DUFLOS A.
HAEUW J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ADZ67084
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(LEGE/)
                                                                                                                                                                                                                                                                    (DUFL/)
(HAEU/)
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New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.

(FABR ) FABRE MEDICAMENT SA PIERRE.

Corvaia N,

Goetsch L,

WPI; 2003-569653/53.

18-JAN-2002; 2002FR-0000654. 18-JAN-2002; 2002FR-00000653

20-JAN-2003; 2003WO-FR000178

WO2003059951-A2.

24-JUL-2003

Homo sapiens.

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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
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Pred. No. 1.1e-47;
3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 83; 164pp; French.
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RESULT 10

KPSLKDRITISRDTSKNOFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117 

61

1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY 

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Gaps ;

Indels

Matches 115; Conservative

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Local Similarity

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                                                                                                                                                                                                     neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
                                                                                                                                                                                       Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)
                                                                                                                                            Human antibody 7C10 3 heavy chain variable region SEQ ID NO:83.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beck A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haeuw J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 13; SEQ ID NO 83; 125pp; English.
                       ADZ67087 standard; protein; 117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leger O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; 2002FR-0000654.
; 2002FR-00005753.
; 2003WO-FR000178.
; 2003FR-00008538.
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                                                                                                      (first entry)
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CORVAIA N.
LEGER O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DUFLOS A. HAEUW J.
                                                                                                                                                                                                                                                                                                                                                                                               US2005084906-A1.
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07-MAY-2002;
20-JAN-2003;
11-JUL-2003;
                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                                        30-JUN-2005
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                                                               ADZ67087;
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(HAEU/)
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    ADZ67087
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preparation of a medicament intended for the prevention or for the treatment of psoriasis. (I) is useful in preparation of a medicament intended for the prevention of a medicament intended for the specific targeting of a biologically active compound to cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I) is useful for in vitro diagnosis of illnesses induced by an overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (I), which is optionally labeled. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ingulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KPSLKDRITISRDTSKNQFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 117;
                                                                                                                                                                                                                                                                                                                                          sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.3%; Score 611; DB 9;
96.6%; Pred. No. 1.1e-47;
ive 3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 85; 164pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic; antipsoriatic; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (FABR ) FABRE MEDICAMENT SA PIERRE
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07-MAY-2002; 2002FR-00005753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-569653/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003059951-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; heavy chain variable region.
           these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IER, and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
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hyperactivity of signal transduction pathways mediated by interaction of
                                                                                                                                                                                                                                         78
                                                                                                                                                                                                                                                                                     KPSLKDRVTISVDTSKNOPSLKLSSVTAADTAVYYCARYGRVFPDYWGQGTLVTVSS 135
                                                                                                                                                                                                                                                                   61 KPSLKDRITISRDTSKNQPSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                             QVQLQESGPGLVKPSETLSLTCTVSGYSISGGYLMNWIRQPPGKGLEWIGYISYDGTNNY
                                                                                                                                                                                                              1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
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                                                                                                                                                     Length 135;
                                                                                                                                                                                  1; Indels
                                                                                                                                                       97.3%; Score 611; DB 7; 96.6%; Pred. No. 1.3e-47;
                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "leader peptide"
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                                                                                                                                                                                                                                                                                                                                                                     ADZ67089 standard; protein; 135 AA
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--- "CDR1"
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; 2002FR-00005753.
; 2003WO-FR000178.
; 2003FR-00008538.
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/note= "CDR2"
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/note= "CDR3"
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                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                  Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note=
                                                                                                                                                                     Best Local Similarity
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CORVAIA N.
LEGER O.
DUFLOS A.
HAEUW J.
BECK A.
                                                                                                                            Sequence 135 AA;
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20-JAN-2003;
11-JUL-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                 ADZ67089;
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                                                                                                                                                       Query Match
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(BECK/)
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The invention relates to a novel isolated anti-inalin-like glowin ractor of receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of applicably inhibiting tyrosine kinase activity of the erceptor, comprising a light or heavy chain having at least one complementary of the average of the fully defined is amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illuses connected with an overexpression and/or an abnormal activation of the IGF-IR and/or softward or EGF, and/or connected with a ctivation of the IGF-IR and/or EGFR, and/or connected with a ctivation of the IGF-IR and/or EGFR, and/or connected with citiation of the IGF-IR and/or EGFR, and/or of EGF with EGFR, where induces accordary effecte connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended conhibit the transformation of normal cells into cells with tumoral character, preferably IGF-dependent, especially IGF-adependent and/or EGF-dependent calls. (I) is useful in the preparation of a medicament intended for prevention or for the treatment of cancer, where the cancer is chosen from prostate cancer, osteosarcoma, lung cancer, the cancer is chosen from prostate cancer, osteosarcoma, lung cancer, conformation or for the preparation of a medicament intended for the prevention or for the preparation of a medicament intended for the prevention or colle sexpension or an underexpression or the abnormal presence, of IGF-call expression or an underexpression of the IGF-IR and/or EGFR receptor; is useful in virto diagnosial sample in which the abnormal presence of IGF-call sample with (I), which is positionally labeled. The present correspondent 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                      The invention relates to a novel isolated anti-insulin-like growth factor
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                                                                                        Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 KPSLKORVTISVDTSKNQPSLKLSSVTAADTAVYYCARYGRVFPDYWGQGTLVTVSS 135
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  Beck
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Pred. No. 1.3e-47;
3; Mismatches 1; Indels
Haeuw J,
Duflos A,
                                                                                                                                                                                                         Example 13; SEQ ID NO 85; 125pp; English.
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Leger O,
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Matches 113; Conservative
Corvaia N,
                                             WPI; 2005-321968/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 135 AA;
Goetsch L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADJ76903;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculloskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; BGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murine immunoglobulin heavy chain variable region 7C10 VH SEQ ID NO:69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 PSLKDRITISRDTSKNOFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein sequence used to generate the Ab of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86.9%; Score 546; DB 7; Le
86.2%; Pred. No. 8.9e-42;
ive 8; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 69; 164pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADZ67073 standard; protein; 117 AA.
                                                                                                                                                                                                                                                                                                                                            (FABR ) FABRE MEDICAMENT SA PIERRE.
                                                                                                                                                                                                                                                                                                                                                                                    Leger 0;
                                                                                                                                                                                                                                                         18-JAN-2002; 2002FR-0000653.
18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-00005753.
                                                                                                                                                                                                                        20-JAN-2003; 2003WO-FR000178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 86.2
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    Goetsch L, Corvaia N,
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-569653/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 117 AA;
                                                                                                                                         WO2003059951-A2.
                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUN-2005
                                                                                                                                                                                24-JUL-2003
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The invention relates to a novel isolated anti-insulin-like growth factor of the invention relates to a novel isolated anti-insulin-like growth factor capable of binding to human IGF-IR and, if necessary, capable of space capable of binding to human IGF-IR and, if necessary, capable of appeal to binding tronslating tyrosine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of amedicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or connected with an activation of the invention of the invention of the medicament does not induce or only slightly induced interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly induced induced in the transformation of normal cells into cells with tumoral character, preferably IGF-dependent, especially IGF1 and/or EGF-dependent, especially IGF1 and/or EGF-dependent and/or HRZ/neu-dependent and/or EGF-dependent and/or HRZ/neu-dependent cells. (I) is useful in the preparation of a medicament intended for prevention or for the treatment of cancer, where the cancer is chosen from prostate cancer, osteosarcome, lung cancer, creatment of a medicament intended for the preparation of a medicament intended for the preparation of a medicament colls. (I) is useful in the preparation of a medicament colls. (I) is useful in preparation of a medicament intended for the special subjection of the IGF-IR and/or EGFR receptor. (I) is useful in preparation of a medicament intended for the specific targeting of a biologically act
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel isolated anti-insulin-like growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (1), which is optionally labeled. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; immunoglobulin; heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Beck A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haeuw J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Duflos A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 13; SEQ ID NO 69; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leger 0,
                                                                                                                                                                                                                                                                     18-JAN-2002; 2002FR-00000653.
18-JAN-2002; 2002FR-00000554.
07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WO-FR000178.
11-JUL-2003; 2003FR-00008538.
                                                                                                                                                                                                                             16-DEC-2003; 2003US-00735916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corvaia N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2005-321968/33.
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                                                                                                                                                                                                                                                                                                                                                                                                          GOETSCH L.
CORVAIA N.
LEGER O.
DUFLOS A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAEUW J.
                                                                                                                                         US2005084906-A1
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                                                                                                  Mus musculus
                                                                                                                                                                                      21-APR-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BECK/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                    (CORV/)
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Sequence 117 AA

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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or-2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or spidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endomerrium and colon, also osteosarcoma, and prostate, lung, breast, andomerrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                VQLQESGPGLVKPSQSLSLITCSVTGYSITGGYLMNWIRQPPGNKLEMMGYISYDGTNNYK
                                                                             VQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNYK
                                                                                                                                                    PSLKDRITISRDTSKNOFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                         Gaps
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   Length 117;
                                       8; Indels
86.9%; Score 546; DB 9;
86.2%; Pred. No. 8.9e-42;
iive 8; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic; antipsoriatic; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (FABR ) FABRE MEDICAMENT SA PIERRE.
                                                                                                                                                                                                                                                                                          ADJ76886 standard; protein; 127 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leger 0;
                                                                                                                                                                                                                                                                                                                                                                                                       Anti-IGF-1R related protein #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-JAN-2002; 2002FR-0000654.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JAN-2002; 2002FR-00000653.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-JAN-2003; 2003WO-FR000178.
                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                       Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goetsch L, Corvaia N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-569653/53
                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 127 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003059951-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus.
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   Query Match
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Length 127;

86.9%; Score 546; DB 7; 86.2%; Pred. No. 9.7e-42;

Query Match Best Local Similarity

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                    61
                            12 VQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNYK 71
                                                         2 VQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNYK
 Gaps
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 Indels
 8
 Mismatches
 ..
80
100; Conservative
 Matches
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Search completed: January 10, 2006, 20:44:17 Job time : 81.7649 secs

us-10-735-916a-75.rpr

OM protein - protein search, using sw model

Run on:

January 10, 2006, 20:28:02; Search time 14.1157 Seconds (without alignments) 797.508 Million cell updates/sec

US-10-735-916A-75 628 1 QVQLQESGPGLVKPSETLSL.......RYGRVFFDYWGQGTLVTVSS 117 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		,			SOUTHERNESS	
Result		Ouerv				
No.	Score	Match	Length	BB	DI	Description
1	505	80.4		7	7782	variable re
7	490	78.0		7		Ig heavy chain V r
m	477	76.0	123	0		Ig heavy chain V r
4	474	75.5		7		Ig heavy chain V r
S	465.5	74.1		~	S24443	Ig heavy chain V r
9	464	73.9		~	831511	Ig heavy chain - h
7	463	73.7	12	~	S37200	Ig heavy chain V r
80	460.5	73.3		0	807637	Ig heavy chain V r
6	459.5	73.2	130	7		Ig heavy chain V r
10	•	73.2	-	7	S31586	Ig heavy chain V r
11	458.5	73.0	116	~	S38718	Ig heavy chain V r
12	458.5	73.0	-	~	S44114	Ig heavy chain V r
13	458	72.9	-	N	S31512	Ig heavy chain - h
14	457.5	72.9		N	S78052	Ig heavy chain pre
15	455.5	72.5		7	\$78055	d
16	455	72.5		~	128195	ď
17	453	72.1		~	S44113	Ig heavy chain V r
18	453	72.1		-	AVMS35	Ig heavy chain pre
19	452	72.0	11	8	E25114	c
20	452	72.0	14	7		Ig heavy chain V r
21	451	71.8		7		Ig heavy chain pre
22	448.5	71.4		~		Ig heavy chain V r
23	448	71.3	14	~	S09711	
24	446.5	•		~		Ig heavy chain V4.
25	444	70.7		~		Ig heavy chain V a
26	443.5	70.6		N		Ig heavy chain V r
27	443	70.5	149	~		Ig heavy chain pre
28	442	70.4	14	~	4770	줌
29	441.5	70.3	134	7	B24672	Ig heavy chain pre

Ig heavy chain pre Ig heavy chain pre Ig heavy chain V	heavy heavy heavy	heavy heavy heavy	Ig lambda chain v Ig heavy chain V r Ig heavy chain V r	Ig heavy chain pre Ig heavy chain V r Ig heavy chain V r Ig heavy chain pre
PL0100 A26340	A23114 F25114 S09710 S12421	S54906 S31696 S26906	S44125 C25114 S30529	B26340 S26902 S19668 A41287
0 00 0	9 10 10 10	000	0 0 0	0000
135	115 115 146 98	134 139 97	105 119 123	116 98 127 139
70.0	69.3	69.1 69.1 68.6	68.6 68.5 68.5	68.3 68.3 68.2
435.5	4.00 4.35 4.35 4.35 4.35	434 434 430.5	430.5 430 430	429.5 429 429 428.5
30	1 E E E	3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0	39 4 4 1 4 0	4 4 4 4 6 6 4 6

## ALIGNMENTS

	RESULT 1
	13/702. 19/702.
	C;Species: Homo sapiens (man)
	C;Date: 16-Feb-1996 #sequence_revision 13-Mar-1997 #text_change 23-Jul-1999
	C;Accession: 137782; S25476
	R;Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.
	Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
	A; Title: Somatic diversification in the heavy chain variable region genes expressed by i
	A;Reference number: A36876; MUID:94119917; PMID:8290556
_	A;Accession: 137782
_	A;Status: preliminary
	A; Molecule type: mRNA
	A;Residues: 1-140 <res></res>
	A; Cross-references: UNIPARC: UP10000176E83; EMBL: X67906; NID: 933582; PIDN: CAA48104.1; PI
_	C;Superfamily: immunoglobulin V region; immunoglobulin homology
	F;46-128/Domain: immunoglobulin homology <1MM>

ä Gaps 8; Query Match 80.4%; Score 505; DB 2; Length 140; Best Local Similarity 81.3%; Pred. No. 3.2e-39; Matches 100; Conservative 6; Mismatches 9; Indels

61 KPSLKDRITISRDISKNOFSLKLSSVTAADTAVYYCAR-----YGRVFFDYWGQGTLVT 114 9 20 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGYIYYSGSTNY 78 1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY 138 VSS 140 115 VSS 117 g g 8 ò g õ

RESULT 2 S31690

Journal of Meany Chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: S31650
R;Culsinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
R;Culsinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
R;Culsinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
R;Culsinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
R;Culsinier, M.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
A;Recreance number: S31585
A;Accession: S31590
A;Accession: S31590
A;Accession: S31590
A;Accession: S31590
A;Accession: S31590
A;Accession: S31590
A;Accession: Manh
A;Residues: 1-130 <CUl.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

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A,Molecule type: mRNA
A,Residues: 1-118 <JON>
A,Cross-references: UNIPARC:UPI0000115FE9; EMBL:X61650; NID:g37720; PIDN:CAA43831.1; PII
R,Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter,
J. Mol. Biol. 222, 581-597, 1991
A,Title: By-passing immunization. Human antibodies from V-gene libraries displayed on pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Molecule type: mRNA
A,Residues: 1-155 <CHA>
A,Cross-references: UNIPARC:UPI00001160FF; EMBL:X69866; NID:g33094; PIDN:CAA49500.1; PII
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords: heterotetramer; immunoglobulin
P;47-129/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S31511
S;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
S;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
S;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
S;Demaitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA A;Accession: S31519
                                                                                                                                                                                                                                  60 YKPSLKDRITISRDTSKNQPSLKLSSVTAADTAVYYCAR----YGRVFFDYWGQGTLVTV 115
                                                                                                                                                                                                                                                                     87 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARPLLWFGEL-FDYWGQGTLVTV 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLQESGPGLVKPSETLSLVCTVSGGSLSFSY-WGWIRQPPGKGLEWIGYISHRGSTDY 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 NSSLQSRVTISADTSKNQFSLKLSSVTAADTAVYYCARSFSNSFFFGYWGQGTLVTVSS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 KPSLKDRITISRDTSKNQFSLKLSSVTAADTAVYYCAR--YGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C, Louis 12-Jan-1993 #Sequence_revision 22-Jan-1993 #text_change 20-Jun-2000 C, Accession: S24443; S19667
R, Jones, P.T.
submitted to the EMBL Data Library, October 1991
A, Reference number: $24442
A, Molecula 189443
                                                                                                                    1 QVQLQESGPGLVKPSETLSLTCTVSGYSI-TGGYLWNWIRQPPGKGLEWMGYISYDGTNN
                                                                                                                                                    27 QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYMGWIRQPPGKGLBWIGSIYYSGSTY
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                                                              Gaps
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     Length 147;
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <1MM>
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                                                           Indels
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                                                                 14;
  Score 474; DB 2;
Pred. No. 2.3e-36;
7; Mismatches 14.
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Best Local Similarity 77.3%; Pred. No. 1.1e-35;
Matches 92; Conservative 8; Mismatches 16
75.5%;
                                Best Local Similarity 77.9
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-55,57-118 <MAR>
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     Query Match
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C;Species: Homo sapiens (man)
C;Accession: S13519
R;Mortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.
Nucleic Acids Res. 19, 673, 1991
AyTitle: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked A;Reference number: S13519
A;Accession: JumyA
A;Residues: 1-147 cMOR>
A;Across-references: UNTPARC;UPIO000115EBBS; EMBL:X56158; NID:g37724; PIDN:CAA39626.1; PIC
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: hetecrotetramer; immunoglobulin
F;41-125/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                             61 KPSLKDRITISRDISKNOFSLKLSSVIAADTAVYYCAR-----YGRV--FFDYWGQGT 111
                                                                                                                                                                                                                                                                                                                              65 NPSLKSRVTISVDISKNOFSLKISSVIAADTAVYYCARGSSVLLWFGELLYYFDYWGQGT 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Homo sapiens (man)
Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
                                                                                                                                                                                                             6 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWSRQPPGKGLEWIGYIYYSGSTNY
                                                                                                                                                                            1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
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                                                                                                                       Gaps
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                                                                 Length 130;
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A;Accession: $30530
A;Accession: $30530
A;Accession: $30530
A;Accession: $30530
A;Residues: 1-123 <MAR>
A;Residues: 1-123 <MAR>
A;Cross-references: UNIPARC;UPI0000176C83; EMBL;Z18316
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                           'Match 78.0%; Score 490; DB 2; Length 13 Local Similarity 77.0%; Pred. No. 7e-38; tes 97; Conservative 8; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: S30530
R;Mariette, X.
submitted to the EMBL Data Library, October 1992
     F;20-102/Domain: immunoglobulin homology <IMM>
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                                                                 Query Match
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
R;Cutsinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the A;Accession: S31586
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C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 YNPSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCARDKGGFWSGYYTRNSRAAFDIW 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 YKPSLKDRITISRDTSKNQFSLKLSSVTAADTAVYYCA------RYGRVFFDYW 107
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                             20 VQLQESGPGLVKPSQSLSLTCSVTDFSITSGYYWHWIRQFFGNKLEWMGYISYDGSNGYN 79
VOLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNYK 61
                                                                                                                                   PSLKDRITISRDISKNOFSLKLSSVTAADTAVYYCAR-YGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGSYYWSWIRQPAGKGLEWIGRIYTSGSTN
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-130 «MRNA»
A;Cross-references: UNIPARC:UPI0000113F45; EMBL:Z18320
C;Superfamily: immunogloblin v region; immunoglobulin homology
C;Superfamily: immunoglobulin immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>
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1 Similarity 71.5%; Pred. No. 4.3e-35, 93; Conservative 7; Mismatches 17
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Best Local Similarity 76.9
Matches 93; Conservative
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Best Local Similarity
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A;Molecule type: mRNA
A;Residues: 1-139 <CUI>
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R; Mariette, X.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sylvour chain V region - mouse
C; Species: Mus musculus (house mouse)
C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
C; Accession: 337200
R; Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.
submitted to the EMBL Data Library, August 1993
A; Reference number: 337200
A; Accession: 537200
C; Superfamily: immunoglobulin V region: immunoglobulin homology
F; 15-98/Domain: immunoglobulin homology < IMM>
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                                                                                                                                           1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY 60
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                                                                                                                                                                                                             33 QVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPPGKGLEWIGYIYYTGSATY
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          Length 155;
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                                                                            14; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 73.7%; Score 463; DB 2; Best Local Similarity 73.3%; Pred. No. 1.9e-35; Matches 88; Conservative 11; Mismatches 17,
   Score 464; DB 2;
Pred. No. 2e-35;
9; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aintrons: 15/3
C;Superfamily: immunoglobulin V region; immunog
C;Kyywords: heterotetramer; immunoglobulin
F;33-116/Domain: immunoglobulin homology <IMM>
       Query Match 73.9%;
Best Local Similarity 75.0%;
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152 TVSS 155
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C;Species: Homo sapiens (man)
C;Accession: 31512
R;Chattagner, P.; Demison, C.; Theze, J.; Zouali, M.
Submitted to the EMBL Data Library, December 1992
A;Abecription: Dominance of clonotypic patterns and variable gene usage of anti-DNA autc
A;Accession: 531512
A;Accession: 531512
                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-152 <CHA-
A;Cross-references: UNIPARC:UP100001160F9; EMBL:X69860; NID:g33082; PIDN:CAA49494.1; PIC
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;47-129/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-140 cHRN-
A; Residues: 1-140 cHRN-
A; Cross-references: UNIPARC: UP10000115E89; EMBL: X54441; NID: 937815; PIDN: CAA38308.1; PII
R; Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
A; Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and }
patient.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92 NPPIKSRVTISVDISKNQPSLKVSSVTAADTAVYYCARGGGISSWYVYYGMDVWGQGTTV 151
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CiSpecies: Homo sapiens (man)
CiDate: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
CiAccession: SY8052; S23717
RiHarindranath, N.
Submitted to the EMBL Data Library, August 1990
A;Reference number: S78051
A;Accession: S78052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
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A;Residues: 15-111 <HAW>
A;Residues: 15-111 <HAW>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72.9%; Score 457.5; DB 2; Length 1 nilarity 71.7%; Pred. No. 7.1e-35; Conservative 9; Mismatches 16; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 458; DB 2;
Pred. No. 7.1e-35;
8; Mismatches 17;
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Best Local Similarity 73.4%;
Matches 91; Conservative
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nes 91; Conserv
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                                                                                                             Ig heavy chain - human
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C;Date: 13.-Zan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Date: 13.-Zan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Accession: 844114
S;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
S;Ubmitted to the EMBL Data Library, March 1994
A;Description: 1diotypic vaccination against human B-cell lymphoma: rescue of variable A;Recreance number: 844105
A;Recreance number: 844105
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-129 cHAW>
A;Residues: 1-129 cHAW>
A;Cross-references: UNIPARC:UPI0000116639; EMBL;Z31579; NID;g472968; PIDN:CAA83451.1; P
                                                                                                                                                                                                                                                                        Johnston V region - mouse

GiSpecies: Mus musculus (house mouse)

Richanis, A.Y.

Richanis, Muscula Library, November 1993

A; Rocession: S38718

A; Rocession: S38718

A; Reference number: S38718

A; Residues: 1-116 < CIM>
A; Constructions: UNIPARC: UPI0000117542; EMBL: X76018; NID: 9416102; PIDN: CAA533605.1; ECS Sylvards: heteroterramer; immunoglobulin homology

C; Roywords: heterotetramer; immunoglobulin homology < IMM>
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61 KPSLKDRITISRDTSKNOFSLKLSSVTAADTAVYYCARYGRVF-----FDYWGQGTLV 113
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Pred. No. 4.7e-35;
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Best Local Similarity
Matches 87; Conserv
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Apacession: S78051
A; Accession: S78055
A; Residues: 1-145
A; Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
A; Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
patient.
A; Reference number: S23716; MUID:92031262; PMID:1718404
A; Recession: S2370
A; Molecule type: mRNA
A; Residues: 18-115
A; Residues: 18-115
A; Residues: 18-115
A; Residues: UNIPARC:UPIO0001769D2; EMBL:X54445
A; Crossrefamily: immunoglobulin V region; immunoglobulin homology
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: immunoglobulin V region; immunoglobulin homology
C; Keywords: immunoglobulin homology < IMM>
F; 1-17/Domain: signal sequence (fragment) #status predicted < S1G>
F; 1-17/Domain: immunoglobulin homology < IMM>
A; Residues: 19 homology < IMM>
A; Residues: 19 homology < IMM>
A; Residues: 10 homology < IMM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig heavy chain precursor V-D-J region (clone mAB 67VH) - human (fragment) C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Sate: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999 C; Accession: S78055; S23720 R; Harindranath, N. Submitted to the EMBL Data Library, August 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
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Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
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"Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype.";
J. Exp. Med. 174:1639-1652(1991).
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01-MAY-2000 (TrEMBLrel. 13, Latt sequence update)
01-MAX-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
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Clin. Immunol. Immunopathol. 87:184-192(1998)
Q53VQ9_MOUSE
Q53VRE_MOUSE
Q51OL9_RAT
Q53VR2_MOUSE
Q58M39_RAT
Q53VQ0_MOUSE
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Q7Z3Y6 HUMAN
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EMBO J. 8:3741-3748(1889).
EMBL, AF035041, AAD56277.1; -; mRNA.
PIR; PH0876; PH0876.
PIR; S12416; S12416.
HSSP; P01820; 1G7J.
SMR; O9UL73; 1-119;
InterPro; IPR007110; Ig-like.
InterPro; IPR00716; Ig-v.
SMARI; SM00406; IGv; I.
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PubMed=1660528;
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PubMed=2511001;
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Copyright (c) 1993 - 2006 Compugen Ltd.
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06LBQE MOUSE

06LBQE MOUSE

06GWX7_HUWAN

HV46_MOUSE

053 VGE MOUSE

059 973_HUWAN

072379_HUWAN

072374_HUWAN

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072374_HUWAN

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RIAUSENER R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsich F.,

Diatchenko L., Marusina K.F., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K.F., Farmer A.A., Rubin G.M., Hong L.,

Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.B.,

Raba S.B., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robar S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Radan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Radan A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

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Shutterfield Y.S. M., Krzywinski M.I., Skalska U., Smailus D.E.,

B. Butterfield Y.S. M., Krzywinski M.I., Skalska U., Smailus D.E.,

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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
SEQUENCE 465 Aa; 51083 MW; B3A9B7D0FDB1386E CRC64;
                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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PROSITE; PS00290; IG MHC; UNKNOWN 2.
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Interpro; IPR003506; Ig MHC.
Interpro; IPR003506; Ig W.
Pfam; PF07654; Cl.set; 3.
SMART; SM00407; IG21; 3.
SWART; SM00407; IG21; 3.
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Klausherg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,

A Lischul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Lapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., WcKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Murny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Kettemen M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Rodriguez A.C., Grimwood J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J.W., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J.W., Schmutz M.N.,

Schnerthon and initial analysis of more than 15,000 full-length human
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                                                                                   61 KPSLKDRITISRDISKNOFSLKLSSVIAADIAVYYCARYGRVFFDYWGQGTLVTVSS 117
                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CO, GO:000382; F:antigen binding; IEA.

CO, GO:000382; F:antigen binding; IEA.

InterPro; IPR003106; Ig-like.

InterPro; IPR00306; Ig-MHC.

InterPro; IPR003596; Ig-V.

FEAN; PR007654; Cl-set; Z.

SWART; SW00406; IGV, I.

FROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS02209; IG_MHC; UNKNOWN_2.

FROSITE; PS02209; IG_MHC; UNKNOWN_2.

FROSITE; PS02209; IG_MHC; UNKNOWN_2.

FROSITE; PS02209; IG_MHC; UNKNOWN_2.

FROSITE; PS02209; IG_MHC; UNKNOWN_2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Mix FVB/N;
TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002031; AAH02091.1; -; mRNA.
HSSP; P01820; 1G7J.
                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                       479 AA.
                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                       Q99M22_MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOC238447 protein.
Name=LOC238447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Mix FVB/N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
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80 YNPSLKSRVTISLDTSKRQFSLKOMSVTAADTAVYFCARAGVWGSFRSWAIDGFNIWGQG 139
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WEDLINE=90067954; PubMed=2587273;

WEDLINE=90067954; PubMed=2587273;

Urakov D.N., Deev S.M., Polyanovsky O.L.;

Urakov D.N., Deev S.M., Polyanovsky O.L.;

WICHECT Acids Res. 17:9481-9481(1989).

WICHECT Acids Res. 17:9481-9481(1989).

REMBL; X16740; CAA34714.1; -; Genomic_DNA.

REMBL; X16740; IQ.

REMBL; X16740; IQ.

REMBL; X16740; IQ.

REMBL; SW00409; IG.

REFERO; IPR003596; IG.

REFERO; IPR003596; IG.

REFERO; SWART; SW00406; IG.; I.

REFERO; REFERO; IG.; I.

REFERO; IG.; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNYK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSLKDRITISRDTSKNOPSLKLSSVTAADTAVYYCAR-YGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 VQLQESGPGLVKPSQSLSLTCSVTDFSITSGYYWHWIRQFPGNKLBWMGYISYDGSNGYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=FVB/N; TISSUE-Colon;
MEDLINE-2238825; PubMed=1247932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 136 AA; 15307 MW; 5B0F439CCFB15C3A CRC64;
                                                                                                                                                                                                                                                                                                                                                              05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 460.5; DB 2
Pred. No. 1.4e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-2005 (TrEMBLrel. 29, 01-FEB-2005 (TrEMBLrel. 29, 01-FEB-2005 (TrEMBLrel. 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VH gene product (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87; Conservative
                                                                                                                                                                                                                                                                                                        QELBQS MOUSE PRELIMINARY;
QGLBQS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q5U413 MOUSE PRELIMINARY;
Q5U413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                            TLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOC544903 protein.
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                                                                                                                                     140 TMVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=LOC544903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62
                                                                                            111
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                                                                                                                                                                                                                                           RESULT SEED OF SEED OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
A phopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Frange C.,
A Brownstein M.J., Usdin T.B., Toobhyuki S., Carninci P., Frange C.,
Braa S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Boaks S.A., McKernan N.J., Maramed J.H., Gupting C.,
A Richards S., Worley K.C., Hale S., Garchen B.J., Lu X., Glibbs R.A.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Brand D.M., Schain J.E., Jones S.J.M., Marra M.A.,
Brand D.M., Schain J.E., Jones B.J.M., Marra M.A.,
Brand D.M., Schain J.E., Jones B.J.M., Marra M.A.,
Brand D.M., Schain J.E., Jones B.J.M., Marra M.A.,
Brand D.M., Brand D.M., Brand D.M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGDYYWSWIRQPPGKGLEWIGXIYYSGSTY 79
                                                                                                                                                                                                                                                                                                        05-JUL_2004 (TrEMBLrel. 27, Created)
05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Hypothesical protein.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGG-YLWNWIRQPPGKGLEWMGYISYDGTNN
                                                                  80 PSLKARISITRDISKNQFFLKINSVITEDTATYYCASRGYSWFPNWGQGTLVIVSA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases. EMBL, BC073773; AAH73773.1; -; mRNA. GO: 0016021; C:integral to membrane; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 73.7%; Score 463; DB 2; Similarity 72.4%; Pred. No. 3.1e-39; 92; Conservative 12; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003599; IG.
InterPro; IPR003599; IG.
InterPro; IPR003599; IG.
InterPro; IPR003596; IG_HRC.
InterPro; IPR003596; IG_HRC.
InterPro; IPR003596; IG_WRC.
InterPro; IPR003596; IG_WRC.
InterPro; IPR003596; IG_W.
Pfam; PF07654; C1-8et; 3.
SWART; SW00409; IG; 2.
SWART; SW00406; IGv; 1.
PROSITE; PS00290; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                        QGGMX1 HUMAN PRELIMINARY;
QGGMX1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA
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                                      62
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 VQLQESGPDLVKPSQSLSLTCTVTGYSITSGYGWHWIRQFPGNKLEWMGYISYSGSNNYN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 PSLKSRISITRDISKNOFFLOLNSVITEDIATYYCARYEGNYDYAMDYMGGGTSVTVSS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 PSLKDRITISRDTSKNOFSLKLSSVTAADTAVYYCARYGRVF---FDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Schaefer C.F., Bhat N.K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
STRAIN=FVB/N; TISSUE=Colon;
NIH MGC Project;
Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPARAL; SENDENCE, IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 2.
SEQUENCE 483 AA; 52714 MW; 7C272DAS01A4A0D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, BC08512, AAH85312.1; -; mRNA.
Ensembl, ENSMUSG000054328; Mus musculus.
GO, GO.003823, F: snatigen binding; IEA.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003566; Ig.
Feam; PF07654; Cl-set; Z.
SMART; SM00409; IG; 3.
SMART; SM00407; IGC1; 3.
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Altschul S.F., Zeeberg B., Buetow K.H.,
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QGGMX7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            cDNA sequences.
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Stapleton M., Soares M.B., Bondlon M.F., Casavant T.L., Scheetz T.E., Brownstein M.J. Ugdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rouffard G.G., Millalon D.K., Muzny D.W., Green B.D., Dickson M.C., Shevchenko Y., Bouffard G.G., Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Anterfield Y.S. N., Krzywinski M.I., Schalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; Tand mouse cDNA sequences.", The proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-701.1986 (Rel. 01, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
10 heavy chain V region MOPC 315 precursor.
MANS musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
MANTOGRAM, MALTIGAE; MALTIMAE; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberger R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073765; AA473765.1; -; mRNA.
EMBL; BC073765; AA473765.1; -; mRNA.
R SMR; QGGMX7; 24-455.
GO; GO:0016021; C:integral to membrane; IEA.
InterPro; IPR003599; Ig.
R InterPro; IPR003100; Ig.
R InterPro; IPR003597; Ig.
R InterPro; IPR003597; Ig.
R InterPro; IPR003597; Ig.
R InterPro; IPR003596; Ig.
R Pfam; PF07654; C1-8et; Z.
R SMART; SM00409; IG; 4.
R SMART; SM00409; IG; 4.
R SMART; SM00409; IG; 4.
R RROSITE; PS00395; IG_MHC; UNKNOWN_2.
R PROSITE; PS00290; IG_MHC; UNKNOWN_2.
R PROSITE; PS00290; IG_MHC; UNKNOWN_2.
R PROSITE; PS00290; IG_MHC; UNKNOWN_2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.0%; Score 458.5; DB 2
75.8%; Pred. No. 9.1e-39;
ive 11; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . Immunol. 26:431-434(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91; Conservative
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PROTEIN SEQUENCE OF 1-31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
TISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
NUCLEOTIDE SEQUENCE.
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P01822:
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62 PSLKDRITISRDTSKNQFSLKLSSVTAADTAVYYCA----RYGRVFF---DYWGQGT 111
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Harindranath N., Goldfarb I.S., Ikematsu H., Burastero S.E., Wilder R.L., Notkins A.L., Casali P.; "Complete sequence of the genes encoding the VH and VL regions of low-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VOLOESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNYK
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                                                                                                                                                                                                                                                                                                                                                           MEDILINE=86136012; PubMed=3937730;
Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic) antibodies in the GAT system.";
                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
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"Clonal proliferation of 1gM secreting B cell in the synovium
Behcet's patient with arthritis.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; Indels
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FOUGGERAU M.;
Submitted UN. 1986) to the EMBL/GenBank/DDBJ databases.

EMBL; X03378; CAA27095.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 AA; 13931 MW; 502E51A5213F056E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VH4 heavy chain variable region precursor (Fragment)
                                                                                                                                                      13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
VH-D-JH region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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Pred. No. 9.4e-39;
                                                                                                                    119 AA
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                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72.0%;
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                                                                                                                   QS3VQ5 MOUSE PRELIMINARY;
Q53VQ5;
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                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=1718404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1999
01-MAR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 VQLQESGPGLVKPSQSLSLTCSVTGXSITSGYFWNWIRQFPGNKLEWLGFIKYDGSNGYN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VOLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNYK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 PSLKDRITISRDTSKNQFSLKLSSVTAADTAVYYCA--RYGRVFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                        (alpha) chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Gaps
                                                                                                                                                                             precursors.";
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE REVISION TO 53.

MEDLINE=77244979; PubMed=268248;
Med L., Margolies M.N., Givol D., Zakut R.;
Unpublished results, cited by:
Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;
Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).

-! MISCELLANEOUS: This alpha chain was isolated from a myeloma protein that has anti-dinitrophenyl activity.
                         Jilka R.L., Pestka S., "Amino acid sequence of the precursor region of MOPC-315 mouse immunoglobulin heavy chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       heavy chain V region MOPC 315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.1%; Score 453; DB 1; Length 137; ilarity 70.3%; Pred. No. 8.6e-39; Conservative 15; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         By similarity.
6 -> 6G (in Ref. 1; CAA30727).
6 -> H (in Ref. 2).
6Y -> YG (in Ref. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complementarity-determining-1. Framework-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complementarity-determining-3.
Pramework-4.
                                                                                                                                                                                                                                                               Francis S.H., Leslie R.G.Q., Hood L., Eisen H.N.; "Amino-acid sequence of the variable region of the heavy of a mouse myeloma protein with anti-hapten activity."; Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15399 MW; FB3828304C2B81DC CRC64;
                                                                                                                                    MEDLINE=79148758; PubMed=428562;
Schechter I., Wolf O., Zemell R., Burstein Y.;
Structure and function of immunoglobulin genes and
Fed. Proc. 38:1839-1845(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N -> D (in Ref. 4).
Missing (in Ref. 4).
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PROSITE; PSS0835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region; Signal.
                                                                               Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696 (1977)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ensembl; ENSMUSG0000057048; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR001596; Ig_v.
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EMBL; X07880; CAA30727.1; -; Genomic_DNA
                                                                                                                                                                                                                                                     MEDLINE=74170779; PubMed=4524622;
         MEDLINE=78094475; PubMed=414225;
                                                                heavy chain."
                                                                                                                                                                                                                                    PROTEIN SEQUENCE OF 19-136.
                                                                                                                      PROTEIN SEQUENCE OF 1-21
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68
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123
137
137 AA;
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SMR; P01822; 20-137
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Best Local Similarity
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Rlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A plokins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A papleton M., Soarse M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKwan P.J., McKernan R.J., Malek J.A., Gunazatne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glubbs R.A.,
A Whiting M., Madan A., Young A., Sodergren E.J., Low, Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Bronezten A., Schein J.B., Jones S.J.M., Marra M.A.,
Bronezten A., Schein J.B., Jones S.J.M., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLQESGPGLVKPSETLSLTCTVSGYSITG-GYLWNWIRQPPGKGLEWMGYISYDGTNN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 QLQLQESGPGLVKPSETLSLSCTVSGGSISSTNYYWGWIRQPPEKGLEWIGSLANSGSDY 79
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
and high-affinity monoclonal IgM and IgAl rheumatoid factors produced by CD5+ B cells from a rheumatoid arthritis patient.";
Int. Immunol. 3:865-875(1991).
EMBL; ARIO1795; ASC79084.1; -; mRNA.
PIR; $31673; $31673.
PIR; $31673; $28056.
HSSP; PO1820; IG70.
SMR; O95973; 20-147.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
SMART; $M0406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.7%; Score 450.5; DB 2; Length 150; 73.7%; Pred. No. 1.7e-38; ative 11; Mismatches 19; Indels 1
                                                                                                                                                                                                                                                                                                                                             Potential.
VH4 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                             1 19 Potential.
20 >150 VH4 heavy chain variable 3
150 150 MW; 85664E04938AA7C9 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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OGP418 HUMAN PRELIMINARY;
AC G69418 G69418 HUMAN PRELIMINARY;
AC G69418 G69
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Best Local Similarity 73.74
Matches 87; Conservative
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61 KPSLKDRITISRDTSKNOFSLKLSSVTAADTAVYYCARYGRVFF---DYWGQGTLVTVSS 117
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 576;
             EMBL; BC063384; AH63384.1; -; mRNA.

REMBL; BC063384; AH63384.1; -; mRNA.

REMBC#L; ENSGO0000196122; Homo sapiens.

InterPro; IRR003159; Ig.

RITHERPRO; IRR003159; Ig.

RITHERPRO; IRR003159; Ig.

REAM; PRO064; C1-set; I.

RAMRT; SM00409; IG; I.

RAMRT; SM00409; IG; I.

ROSITE; PSS0815; IG LIKE; 4.

RROSITE; PSS0815; IG LIKE; 4.

RROSITE; PSS0815; IG LIKE; 4.

RROSITE; PSS0815; IG LIKE; 4.

REQUENCE 576 AA; 63364 MW; FBB97C949D720F1E CRC64;
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Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp686K04218 (Fragment).
Name=DKFZp686K04218,
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                   71.7%; Score 450.5; DB 2 72.5%; Pred. No. 7.5e-38; rative 10; Mismatches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                      87; Conservative
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RX TISSUE=Primary B-Cells,

RX Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Altechenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Woley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,

RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Willing M., Madan A., Young A.C., Sheychenko Y., Boulfard G.G.,

RA Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Butkesley R.W., Touchman J.W., Schmutz J., Myers R.M.,

RA Butkesley R.W., Touchman J.W., Skenka U., Smailus D.E.,

RA Butkerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Generation and initial analysis of more than 15,000 full-length human

The Mouse CDNA sequences."

The Mouse CDNA sequences."

The Mouse CDNA sequences."
                                       78
                                                                                                                                                                                                                                                                Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
PubMed=1904154;
Noale G.A., Kitchingman G.R.;
Noale G.A., Kitchingman G.R.;
mRNA transcripts initiating within the human immunoglobulin mu heavy chain enhancer region contain a non-translatable exon and are extremely heterogeneous at the 5' end.";
Nucleic Acids Res. 19:2427-2433(1991).
EMBL; BC011857; AAN11857.2; -; mRNA.
 19 QVQLQESGPGLVKPSQTLSLTCTVSGGSIGSGDYFWSWIRQAPGRGLEWMGYIYYSGSTY
                            60 YKPSLKDRITISRDISKNOFSLKLSSVIAADIAVYYCAR---YGRVFFDYWGQGTLVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH MGC Project;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                         620 AA
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SMR; Q96EYO; 27-251.
Ensembl; ENSG0000130076; Homo sapiens.
                                                                                                                                                                                                   Created)
                                                                                                                                                                       PRT;
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InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_Cl.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                      Q96EYO HUMAN PRELIMINARY;
Q96EYO;
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TISSUE-Primary B-Cells;
                                                                                                                                                                                                                                                                                                         Homo.
NCBI_TaxID=9606;
                                                                              S 117
                                                                                                        S 138
                                                                                                                                                                                                                                          IGHM protein.
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92 YSPSLKSRLTIFVDTSKNHFSLRLTSVTAADTAVYYCVRHVEGPYG--WFDPWGQGTLVT 149
                                                                                                                                                                                                                                                                                                                                                                                                         61 KPSLKDRITISRDĮSKNQFSLKLSSVTAADĮAVYYCA----RYGRVFFDYWGQGTLVTVS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                            85
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Bukaryota, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 YKPSLKDRITISRDISKNQFSLKLSSVTAADIAVYYCAR----YGRVFFDYWGQGTLVT
                                                                                                                                                                                                                                                                                                                                 27 QVQLQBSGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQPAGKGLEWIGRIYTSGSTNY
                                                                                                                                                                                                                                                                                                  1 QVQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNY
                                                                                                                                                                                                                                                 Gaps
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Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
Bloecker H., Wiemann S.;
Fobo G., Han M., Wiemann S.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX538077; CAD98001.1; -; mRNA.
HSSP; P01820; 1G7J.
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6
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                                                                                                                                                                                       Length 620;
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69.4%; Score 436; DB 2; Length 49
Best Local Similarity 71.5%; Pred. No. 2e-36;
Matches 88; Conservative 9; Mismatches 18; Indels
                                                                                                                                                                                                                                              19; Indels
SMART; SM00409; IG; 2.
SMART; SM00407; IGcl; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LKE; 5.
PROSITE; PS50290; IG_MHC; UNKNOWN 3.
SEQUENCE 620 Aa; 68125 MW; 990AlA46E8FF27B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last annotation update)
                                                                                                                                                                                          DB 2;
                                                                                                                                                                                       Match 70.6%; Score 443.5; DB 2 Local Similarity 75.2%; Pred. No. 4.3e-37; les 91; Conservative 6; Mismatches 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence upda
01-MAR-2004 (TrEMBLrel. 26, Last annotation up
Hypothetical protein DKFZp686C02218 (Fragment)
Homo sapiens (Human).
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Ensembl; ENSG0000130076; Homo sapiens.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_WHC.
PF007654; C1-set; 2.
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PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Who musculus (Mouse).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia, Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1] — MUCLEOTIDE SEQUENCE. MUCLEOTIDE SEQUENCE. MUCLEOTIDE SEGUENCE. Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.; Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.; The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic) antibodies in the GAT system."; EMBO J. 4:3681-3688(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 69.3%; Score 435.5; DB 2; Length 120; Best Local Similarity 68.1%; Pred. No. 4.8e-37; Matches 81; Conservative 15; Mismatches 14; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fougereau M.; Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases. EMBL; X03375; CAA27077.1; -; mRNA. EMBL; X03374; CAA27071.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 120
120 AA; 13892 MW; 013452306EBAA3BE CRC64;
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NUCLEOTIDE SEQUENCE OF 28-29.
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Search completed: January 10, 2006, 20:53:27 Job time : 79.8731 secs

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January 10, 2006, 20:55:23; Search time 5.96642 Seconds (without alignments) 166.558 Million cell updates/sec
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Cgn2 6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*
Cgn2 6/ptodata/1/pubpaa/PCT NEW PUB.pep:*
Cgn2 6/ptodata/1/pubpaa/USO9 NEW PUB.pep:*
Cgn2 6/ptodata/1/pubpaa/USO1 NEW PUB.pep:*
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GenCore version 5.1.6 (c) 1993 - 2006 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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636
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			1 7	TAAV	App1	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	App	, Ap	2, Appli	, Ap	, Ap	Appl	11, App	ildď	1651, Ap	Appl	Appl
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		Description		aorranhas	Seguence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence				Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence
SUMMARIES		a		02-11-012-333-69	US-11-012-353-52	US-11-012-353-70	-	US-11-012-353-77	US-11-012-353-79	US-11-012-353-81	US-10-512-184-34	US-10-512-184-71	US-10-512-184-49	US-11-012-353-83	US-11-012-353-85	US-11-012-353-71	US-11-009-939-22	US-11-012-353-162	US-11-054-515-1994	US-11-185-615-2	US-11-054-515-1619	US-11-054-515-1548	US-11-012-353-73	US-11-054-515-841	US-11-185-615-4	US-11-054-515-1651	US-10-923-327-13	US-10-923-327-18
		DB			_	7	7	7	7	7	9	9	9	7	7	7	-	7	7	7	7	7	7	7	7	7	9	9
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	æ	Query Match		7007	100.0	89.5	85.8	82.8	85.1	85.1	84.8	84.8	84.8	83.2	83.2	78.2	76.8	73.4	64.9	64.2	63.7	63.3	62.9	62.7	62.4	62.2	62.1	62.1
		Score		979	636	569.5	546	546	541	541	539.5	539.5	539.5	529	529	497.5	488.5	467	412.5	408	405	402.5	400	399	397	395.5	395	395
		Result No.		-	7	Э	4	5	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Sequence 7, Appli Sequence 72, Appli Sequence 139, Ap Sequence 1361, Ap Sequence 1578, Ap Sequence 1578, Ap Sequence 1597, Ap Sequence 100, Appl Sequence 100, Appl Sequence 17, Appli Sequence 1607, Ap Sequence 1607, Ap Sequence 1607, Appli Sequence 1607, Appli	Sequence 11, Appl Sequence 1960, Ap
US-10-923-327-7 US-10-923-327-9 US-11-012-353-79 US-11-054-515-1339 US-11-054-515-1361 US-11-054-515-1361 US-11-054-515-1578 US-11-054-515-1578 US-11-054-515-1597 US-11-054-515-1697 US-11-054-515-1697 US-11-054-515-1697 US-11-054-515-1697 US-11-054-515-1697 US-11-054-515-1697 US-11-128-900-7 US-11-128-900-86 US-10-923-327-14 US-10-923-327-15	US-10-923-327-11 US-11-054-515-1960
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602.1 661.1.8 660.0 660.0 660.0 660.0 70.0 70.0 70.0	59.7 59.7
395 3993 3993 3993 391 394 394 394 394 394 394 394 396 396 396 396 396 396 396 396 396 396	380 379.5
27 27 27 28 28 28 28 28 28 28 28 28 28 28 28 28	44 5 5

## ALIGNMENTS

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TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

FILE REFERENCE: 01773-198

CURRENT APPLICATION NUMBER: US/11/012,353

CURRENT PILING DATE: 2004-12-16

PRIOR APPLICATION NUMBER: RR 0308538

PRIOR APPLICATION NUMBER: RR 0308538

PRIOR APPLICATION NUMBER: RR 0308538

PRIOR FILING DATE: 2003-07-11

PRIOR APPLICATION NUMBER: FR 0205753

PRIOR FILING DATE: 2003-07-07

PRIOR FILING DATE: 2002-01-20

PRIOR FILING DATE: 2002-01-20

PRIOR FILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18

PRIOR APPLICATION NUMBER: FR 020653

PRIOR FILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18

NUMBER OF SEQ ID NOS: 162

SOUTHWARE: PATCHILL OF NOS: 162

SOUTHWARE: PATCHILL OF NOS: 162
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100.0%; Pred. No. 8.9e-51;
tive 0; Mismatches 0;
Sequence 69, Application US/11012353
Publication No. US20050249730A1
GENERAL INFORMATION:
APPLICANT: GORTSCH, LILIANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: LEGER, OLIVIER
APPLICANT: BECK, ALAIN
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Best Local Similarity 100.
Matches 117; Conservative
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LENGTH: 117
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Publication No. US20050249730A1

GENERAL INFORMATION:

APPLICANT: CORVAIA, NATHALIE

APPLICANT: DUFLOS, ALAIN

APPLICANT: BECK, ALAIN

APPLICANT: BECK, ALAIN

APPLICANT: BECK, ALAIN

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND USES THEREOF

FILE REFERENCE: 017753-196

PRIOR PLICATION NUMBER: 10/735,916

PRIOR FILING DATE: 2003-07-11

PRIOR PLILNG DATE: 2003-07-11

PRIOR PLILNG DATE: 2003-01-20

PRIOR FILING DATE: 2003-01-20

PRIOR APPLICATION NUMBER: FC OFF03)

PRIOR FILING DATE: 2003-01-20

PRIOR APPLICATION NUMBER: FC OFF03)

PRIOR FILING DATE: 2003-01-20

PRIOR APPLICATION NUMBER: FC OFF03)
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S-11-012-353-52
Sequence 52, Application US/11012353
Sequence 52, Application US/11012353
Sequence 52, Application WS/11012353
Sequence 52, Application WS/11012353
SEQUENCE OF US20050249730A1
SAPLICANT: GOSTSCH, LILIANE
APPLICANT: DUFLOS, ALAIN
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: BECER, OLIVIER
APPLICANT: BECK, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 636; DB 7; Length 127; Best Local Similarity 100.0%; Pred. No. 9.6e-51; Matches 117; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              TITLE REPERRUCE: 017753-198
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT FILING DATE: 2004-12-16
PRIOR PILING DATE: 2004-12-16
PRIOR FILING DATE: 2003-12-16
PRIOR FILING DATE: 2003-01-11
PRIOR PLING DATE: 2003-01-11
PRIOR PLING DATE: 2003-01-11
PRIOR PLING DATE: 2003-01-10
PRIOR PLING DATE: 2003-01-20
PRIOR PLING DATE: 2003-01-20
PRIOR PLING DATE: 2002-05-07
PRIOR PLING DATE: 2002-05-07
PRIOR PLING DATE: 2002-01-18
SOUTHWARE: PATENTING DATE: 2002-01-18
PRIOR PLING DATE: 2002-01-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) ORGANISM: Mus musculus
US-11-012-353-52
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WESOUR

Sequence 75, Application US/11012353

Sequence 75, Application US/11012353

Publication Wo. US20050249730A1

GENERAL INFORMATION:

APPLICANT: GOETSCH, LILIANE

APPLICANT: DUFLOS, ALAIN

APPLICANT: BECK, ALAIN

APPLICANT: BECK, ALAIN

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: NOVEL ANTI-O12,353

CURRENT APPLICATION NUMBER: US/11/012,353

CURRENT APPLICATION NUMBER: US/11/012,353

CURRENT APPLICATION NUMBER: PROJESSE

PRIOR PLING DATE: 2003-07-11

PRIOR PLING DATE: 2003-07-11

PRIOR PPLICATION NUMBER: FR 0205553

PRIOR PLING DATE: 2003-01-20

PRIOR PLING DATE: 2002-02-07

PRIOR PLING DATE: 2003-01-18

PRIOR PLING DATE: 2002-01-18

PRIOR PLING DATE: 2002-01-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 NPSLKORISITRDTSKNQFFLKLNSVTTEDTATYYCAREGYGYFFDYWGQGTTLTVSS 118
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PRIOR FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: FR 0200653
PRIOR PILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 0200654
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARE: Patentin Ver: 3.3
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SOFTWARE: Patentin Ver. 3.3
                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Mus musculus
US-11-012-353-70
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US-11-012-353-75
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Query Match
Best Local Similarity
Matches 98; Conserv
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               Sequence 77, Application US/11012353
Publication No. US2005024973041
GENERAL INFORMATION:
APPLICANT: GORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
APPLICANT: BECK, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
FRIOR PLILING DATE: 2004-12-16
PRIOR PLILING DATE: 2003-01-20
PRIOR PPLICATION NUMBER: FR 0200553
PRIOR PLILING DATE: 2002-01-20
PRIOR PLILING DATE: 2002-01-20
PRIOR PLILING DATE: 2002-01-18
PRIOR PLILING DATE: 2002-01-18
PRIOR PLILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR PLILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
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APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: LEGEW, OLLVIER
APPLICANT: BECK, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGP-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
TITLE OF INVENTION: NUMBER: US/11/012,353
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT APPLICATION NUMBER: 10/735,916
PRIOR PILING DATE: 2003-12-16
PRIOR PLING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: PCT/FR03/00178
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-07-11
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86.2%; Pred. No. 1.1e-42;
tive 8; Mismatches 8;
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; Sequence 79, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 86.2
Matches 100; Conservative
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CORGANISM: Homo sapiens
US-11-012-353-77
US-11-012-353-77
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Sequence 81, Application US/11012353

| Sequence 81, Application US/11012353
| Publication No. US20050249730A1
| GENERAL INFORMATION:
| APPLICANT: CORVAIA, NATHALIE
| APPLICANT: CORVAIA, NATHALIE
| APPLICANT: CORVAIA, NATHALIE
| APPLICANT: LEGEN, OLIVIER
| PRICE OF INVENTION: NECEFORS ANTIBODIES AND USES THEREOF
| TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
| TITLE OF INVENTION: NUMBER: US/11/012,353
| CURRENT APPLICATION NUMBER: 10/735-916
| PRICE FILING DATE: 2003-07-11
| PRICE FILING DATE: 2003-07-11
| PRICE FILING DATE: 2003-07-11
| PRICE FILING DATE: 2002-01-08
| PRICE FILING DATE: 2002-01-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 117;
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84.5%; Pred. No. 2.7e-42;
ative 10; Mismatches 8
PRIOR APPLICATION NUMBER: FR 0205753
PRIOR FILING DATE: 2002-05-07
PRIOR PRING DATE: 2002-01-05
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 0200654
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARE: PATENTIN Ver. 3.3
SEQ ID NO 79
LENGTH: 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98; Conservative
                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT; ORGANISM: Homo sapiens
US-11-012-353-79
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Sequence 83, Application US/11012353

Publication No. US20050249730A1

GENERAL INCOMATION:
APPLICANT: GORYATION:
APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: ARGEN, OLIVIER
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULING DATE: 2004-12-16
PRIOR FILING DATE: 2003-12-16
PRIOR FILING DATE: 2003-07-11
115 DVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYYWNWIRQFPGNKLEWMGYISYDGTNNN 174
                                                                                                            US-10-512-184-49

Sequence 49, Application US/10512184

Sequence 49, Application US/10512184

Publication No. US20050244901A1

GENERAL INFORMATION:

APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung (
TITLE OF INVENTION: Antibody fragments and fusions mediated plant disease;

TITLE OF INVENTION: Antibody fragments and fusions mediated plant disease;

TITLE OF INVENTION: Antibody fragments and fusions mediated plant disease;

TITLE OF INVENTION: NUMBER: US/10/512,184

CURRENT APPLICATION NUMBER: US/10/512,184

CURRENT FILING DATE: 2004-10-22

NUMBER OF SEQ ID NOS: 72

SOPTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      404 NPSLKNRISITRDASKNQFFLKCINSVTTEDTATYHCARGAPYYGKGTWFPYWGQGTLVTV
                                                                               61 KPSLKDRISITRDTSKNOFFLKLNSVTNEDTATYYCAR----YGR-VFFDYWGQGTTLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: fusion protein OTHER INFORMATION: comprising the leader peptide - chitinase- linker OTHER INFORMATION: - scFv PL2 - cmyc/His6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 539.5; DB 6
Pred. No. 1.8e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial Sequence
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US-10-512-184-49
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US-11-012-353-83
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LENGTH: 626
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TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: resistance against fungi
FILE REFERENCE: 3581.01US01
CURRENT APPLICATION UNDER: US/10/512,184
CURRENT PILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 71
LENGTH: 371
                                                                                                                                Sequence 34, Application US/10512184
Publication No. US20050244901A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL SET OF INVENTION:
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant antibodies, recombinant TITLE OF INVENTION: Antibody fragments and fusions mediated plant disease TITLE OF INVENTION: resistance against fungi
FILE REFERENCE: 3581.01US01
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
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     80 PSLKDRVTISRDTSKNOFSLKLSSVTAADTAVYYCARYGRVFFDYWGQGTLVTVSS 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: scFv PL2 with OTHER INFORMATION: specificity against Phoma lingam; originates from OTHER INFORMATION: Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: precursor OTHER INFORMATION: fusion protein comprising ACE - linker - OTHER INFORMATION: SCFV PL2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 6; Length 259;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 84.8%; Score 539.5; DB 6; Best Local Similarity 84.4%; Pred. No. 7.8e-42; Matches 103; Conservative 5; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 71, Application US/10512184
Publication No. US20050244901A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 34
LENGTH: 259
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                                                                                        RESULT 8
US-10-512-184-34
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Gaps

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US-11-012-353-71

i Sequence 71. Application US/11012353

i Publication No. US20050249730A1

j GENERAL INFORMATION:

APPLICANT: GOETSCH, LILIANE

APPLICANT: GOETSCH, LILIANE

APPLICANT: CORVAIA, NATHALIE

APPLICANT: DUFLOS, ALAIN

APPLICANT: BECK, ALAIN

TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

TITLE OF INVENTION: NUMBER: US/11/012,353

CURRENT FILING DATE: 2004-12-16

PRIOR PELICATION NUMBER: FR 0308538

PRIOR PELICATION NUMBER: FR 0205753

PRIOR PELICATION NUMBER: PR 0205753

PRIOR PELICATION NUMBER: FR 020553

PRIOR APPLICATION NUMBER: FR 020553

PRIOR APPLICATION NUMBER: FR 020553

PRIOR PELICATION NUMBER: PR 020553

PRIOR PELICATION N
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; Sequence 22, Application US/11009939
; Publication No. US20050265998A1
; GENERAL INFORMATION:
   APPLICAWT: Elson, Greg Christopher Andrew
; TILLE OF INVENTION: Neutralizing Antibodies and Methods of Use Thereof
; FILE REFERENCE: 23135-402
; CURRENT APPLICATION NUMBER: US/11/009,939
; CURRENT FILING DATE: 2005-12-10
; PRIOR APPLICATION NUMBER: 60/528,811
; PRIOR FILING DATE: 2003-12-10
; RIOR FILING DATE: 2003-12-10
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 22
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78.2%; Score 497.5; DB 7; Length 118; 81.4%; Pred. No. 2.1e-38; tive 7; Mismatches 14; Indels 1
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US-11-012-353-71
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Best Local Similarity
Matches 96; Conserv
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US-11-012-353-85

j Sequence 85, Application US/11012353

j Sequence 86, Application WS/11012353

j Publication No. US20050249730A1

j GENERAL INFORMATION:

j APPLICANT: GORTSCH, LILIANE

j APPLICANT: DUFLOS, ALAIN

j APPLICANT: HEADY, CHANNER

j APPLICANT: HEADY, CHANNER

j APPLICANT: HEADY, ALAIN

ritte OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

ritte OF INVENTION: NUMBER: 10/735,916

prior APPLICATION NUMBER: 10/735,916

prior APPLICATION NUMBER: 10/735,916

prior PILING DATE: 2003-12-16

prior PILING DATE: 2003-12-16

prior PILING DATE: 2003-07-11

prior PILING DATE: 2003-07-11

prior PILING DATE: 2003-07-11

prior APPLICATION NUMBER: PCT/PR03/00178

prior PILING DATE: 2003-07-11

prior APPLICATION NUMBER: PC0553

prior APPLICATION NUMBER: PC0563

prior 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 83.2%; Score 529; DB 7; Length 117; Best Local Similarity 82.8%; Pred. No. 3.2e-41; Matches 96; Conservative 11; Mismatches 9; Indels
PRIOR APPLICATION NUMBER: PCT/FR03/00178
PRIOR FILING DATE: 2003-01-20
PRIOR APPLICATION NUMBER: FR 0205753
PRIOR PILING DATE: 2002-05-07
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARE: PATENTIN VET. 3.3
LENGTHA: 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
US-11-012-353-83
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Best Local Similarity
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Sequence 162, Application US/11012353

Sequence 162, Application Ws/11012353

Publication No. US20050249730A1

GENERAL INFORMATION:

APPLICANT: CORVAIA, NATHALIE

APPLICANT: CORVAIA, NATHALIE

APPLICANT: CORVAIA, NATHALIE

APPLICANT: DEGEN, OLIVIER

APPLICANT: BEEK, ALAIN

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

FILE REFREENCE: 017753-198

CURRENT APPLICATION NUMBER: US/11/012,353

CURRENT FILING DATE: 2004-12-16

PRIOR FILING DATE: 2003-07-11

PRIOR FILING DATE: 2003-07-11

PRIOR FILING DATE: 2003-07-11

PRIOR FILING DATE: 2002-01-18

NUMBER: PATCHIN VOLE: 3.3

SOFTWARE: PATCHIN VOLE: 3.3
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                                                                                                                                                                                                                                                                                                                                                                             61 NPSLKTRISITRDISKNQFFLQLNSVTTEDTATYXCARKDPSDG---PPYWGQGTLVTVS 117
                                                                                                                                                                                                                                                                      1 DVQLQBSGPDL1QPSQSLSLTCTVTGYSITGGYSWHWIRQFPGNKLBWMGYIHYSGYTDF 60
                                                                                                                                                                                                                                          1 DVQLQESGPGLVXPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNXLEWMGYISYDGTNNY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VOLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNYK 61
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                                                                                                                                                                                        7; Gaps
                                                                                                                             Query Match 76.8%; Score 488.5; DB 7; Length 118; Best Local Similarity 76.9%; Pred. No. 1.3e-37; Matches 93; Conservative 9; Mismatches 12; Indels 7;
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; LENGTH: 118
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-009-939-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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US-11-012-353-162
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Search completed: January 10, 2006, 21:36:23 Job time : 5.96642 secs

Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

Database :

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Sequence 2, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 7, Appli
Sequence 13, Appli
Sequence 131, App
Sequence 131, App
Sequence 131, App
Sequence 29, Appli
Sequence 29, Appli
Sequence 29, Appl
Sequence 21, Appli
Sequence 21, Appli
Sequence 22, Appli
Sequence 22, Appli
Sequence 22, Appli
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                                                                                                                                                                                                                                                                                                                                                                                 Sequence 69, Application US/10735916A

Sequence 69, Application World Sequence 69, Application No. US20050084906A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GORVALA, Nathalie
APPLICANT: UEGER, Ollvier
APPLICANT: DEGER, Ollvier
APPLICANT: DEGER, Ollvier
APPLICANT: HAEUW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
ITLE REPERENCE: 017753-183
CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT FILING DATE: 2003-12-16
FRIOR APPLICATION NUMBER: FR 03/08 538
FRIOR APPLICATION NUMBER: FR 03/08 653
FRIOR APPLICATION NUMBER: FR 02/06 654
FRIOR APPLICATION NUMBER: FR 02/06 654
FRIOR PILING DATE: 2002-01-18
FRIOR PILING DATE: 2002-05-07
NUMBER OF SEQ ID NOS: 156
SEQ ID NO 654
SEQ ID NO 654
SEQ ID NO 655
SEQ ID NO 657
TURNER PATENTING NUMBER: FR 02/05 753
TURNER PATENTING DATE: 2002-05-07
NUMBER OF SEQ ID NOS: 156
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US-10-184-300A-3

US-09-920-171-2

US-10-113-96-2

US-10-113-96-2

US-09-802-077-3

US-09-802-077-3

US-09-925-179-3

US-10-968-237-3

US-10-113-248-7

US-10-741-657A-19

US-10-741-657A-19

US-10-138-29

US-10-10-674-36

US-10-10-674-36

US-10-10-674-36

US-10-10-674-36

US-10-10-674-36

US-10-383-679-12
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US-10-735-916A-52
Sequence 52, Application US/10735916A
; Publication No. US20050084906A1
    1118
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   TYPE: PRT
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Sequence 72, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 77, Appl
Sequence 77, Appl
Sequence 79, Appl
Sequence 79, Appl
Sequence 81, Appl
Sequence 81, Appl
Sequence 82, Appl
Sequence 119, App
Sequence 28, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 26, Appl
Sequence 46, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 270, Appl
Sequence 270, Appl
Sequence 48, Appl
Sequence 70, Appl
Sequence 64, Appl
Sequence 67, Appl
                                                                                                           January 10, 2006, 20:53:43; Search time 64.1754 Seconds (without alignments) 761.757 Million cell updates/sec
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636
1 DVQLQESGPGLVKPSQSLSL......RYGRVFFDYWGQGTTLTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Published Applications AA Main:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                   5.1.6
Compugen Ltd
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US-10-735-916A-52
US-10-735-916A-70
US-10-372-481-17
US-10-373-916A-75
US-10-735-916A-75
US-10-735-916A-75
US-10-735-916A-79
US-10-735-916A-79
US-10-735-916A-83
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US-10-632-706-67
US-10-741-657A-21
US-09-791-551-109
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                                                                                                                                                                                                                                                                                     1867569 segs, 417829326 residues
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                     GenCore version (c) 1993 - 2006
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Maximum Match 100%
Listing first 45 summaries
                                                                               - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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US-10-735-916A-70

Sequence 70, Application US/10735916A

Publication No. US2050084906A1

GENERAL INFORMATION:
APPLICANT: GORYSICH, Liliane
APPLICANT: CORYSICH, Liliane
APPLICANT: CORYSICH, Nathalie
APPLICANT: ELEGER, Olivier
APPLICANT: BEEK, Alain
APPLICANT: BEEK, Alain
APPLICANT: BEEK, Alain
APPLICANT: BOUNCE, ANION
APPLICANT: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
TITLE OF INVENTION: NOVEL ANTI-166

FILE OF INVENTION NUMBER: FR 03/08 538
FRIOR PELLING DATE: 2003-07-11
FRIOR APPLICATION NUMBER: FR 02/00 653
FRIOR APPLICATION NUMBER: FR 02/00 653
FRIOR PELLING DATE: 2002-01-18
FRIOR PELLING DATE: 2002-01-18
FRIOR PELLING DATE: 2002-01-18
FRIOR PELLING DATE: 2002-01-18
FRIOR FILING DATE: 2002-01-18
FRIOR FILING DATE: 2002-01-18
FRIOR FILING DATE: 2002-01-18
FRIOR FILING DATE: 2002-05-07
FRIOR FILING DATE: 2002-01-18
FRIOR FILING DATE: 2003-01-18
FRIOR FILING DATE: 2003-01-18
FRIOR FILING DATE: 2003-01-18
FRIOR FILING DATE: 2003-01-
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                                                               APPLICANT: GORVALA, Nathalie
APPLICANT: GORVALA, Nathalie
APPLICANT: CORVALA, Nathalie
APPLICANT: LEGER, Olivier
APPLICANT: LEGER, Olivier
APPLICANT: BECK, Alain
APPLICANT: WOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REPERENCE: 01773-183
CURRENT FILING DATE: 2003-12-16
PRIOR PELING DATE: 2003-01-11
PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
PRIOR PILING DATE: 2003-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
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100.0%; Score 636; DB 5; Length 127;
Best Local Similarity 100.0%; Pred. No. 4.9e-51;
Matches 117; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Mus musculus
US-10-735-916A-52
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ORGANISM: Mus musculus
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| Sequence 117, Application US/10372481
| Sequence 117, Application US/030202975A1
| Publication No. US20030202975A1
| GENERAL INFORMATION:
| APPLICANT: Tedder, Thomas F.
| TITLE OF INVENTION: REAGENTS AND TREATMENT METHODS FOR AUTOIMMUNE DISEASES
| FILE REFERENCE: 5405.306
| CURRENT FILING DATE: 2003-02-21
| FRIOR APPLICATION NUMBER: US/10/372,481
| CURRENT FILING DATE: 2003-02-21
| PRIOR FILING DATE: 2003-02-21
| PRIOR FILING DATE: 2002-10-21
| PRIOR FILING DATE: 2002-10-21
| PRIOR PLICATION NUMBER: US 60/420,472
| PRIOR PLICATION NUMBER: US 60/359,419
| PRIOR PLICATION NUMBER: US 60/359,419
| SOFTWARE: Patentin version 3.2
| SOFTWARE: Patentin version 3.2
| SOFTWARE: Patentin version 3.2
                                                                                                                                                          1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYYWNWIRQFPGNKLEWMGYINYDGNNNY 60
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                                                                                                                                                                                                                                                                                           61 NPSLKARISITRDTSKAQPFLKLANSVTTEDTATYYCAREGYGYFFDYWGQGTTLTVSS 118
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                                                                                                                                                                                                                                                      61 KPSLKDRISITRDTSKNOFFLKLANSVTNEDTATYYCARYG-RVFFDYWGQGTTLTVSS 117
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                                                              Gaps
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   Length 118;
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| GENERAL INFORMATION:
| APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
| APPLICANT: TESCANO, JOSEPh
| APPLICANT: TESCANO, JOSEPh
| APPLICANT: TEDDER, Thomas
| TITLE OF INVENTION: TREATMENT METHODS USING ANTI-CD22
| TITLE OF INVENTION: ANTIBODIES
| FILE REPERENCE: 39754-0951
| CURRENT APPLICATION NUMBER: US/10/371,797
| CURRENT FILING DATE: 2003-02-21
| PRIOR PILING DATE: 2002-10-21
| PRIOR APPLICATION NUMBER: US 60/420,472
| PRIOR APPLICATION NUMBER: US 60/359,419
| PRIOR PILING DATE: 2002-02-21
| NUMBER OF SEQ ID NOS: 31
| SOFTWARE: PSECSEQ for Windows Version 4.0
| SEQ ID NO 17
                                                              Indels
                                                                                                                             1 DVOLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQF
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Best Local Similarity 87.3%; Pred. No. 5.5e-43;
Matches 103; Conservative 5; Mismatches 9;
Query Match 89.5%; Score 569.5; DB 5; Best Local Similarity 90.7%; Pred. No. 6.4e-45; Matches 107; Conservative 2; Mismatches 8;
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Publication No. US20040001828A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-10-372-481-17
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RESULT 9
US-10-735-916A-79
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                                                                                                                                      9; Indels 1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 75, Application US/10735916A
Sublication No. US20050084906A1
GENERAL INFORMATION:
APPLICANT: GORTSCH, Liliane
APPLICANT: LGGER, Olivier
APPLICANT: LGGER, Olivier
APPLICANT: BECK, Alain
APPLICANT: BECK, Alain
APPLICANT: HAEUW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-183
                                                                                           Query Match 86.2%; Score 548.5; DB 4; Length 118; Best Local Similarity 87.3%; Pred. No. 5.5e-43; Matches 103; Conservative 5; Mismatches 9; Indels 1
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85.8%; Score 546; DB 5;
Best Local Similarity 86.2%; Pred. No. 9.4e-43;
Matches 100; Conservative 8; Mismatches 8;
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CURRENT PELICATION NUMBER: US/10/735,916A
CURRENT FILING DATE: 2003-12-16
PRIOR APPLICATION NUMBER: ER 03/08 538
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-01-20
PRIOR FILING DATE: 2003-01-20
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-05-07
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 75
LENGTH: 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEGER, Olivier
DUFLOS, Alain
BECK, Alain
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CORGANISM: Homo sapiens
US-10-735-916A-75
i TYPE: PRTi ORGANISM: homo sapiensUS-10-371-797-17
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US-10-735-916A-77
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APPLICANT:
APPLICANT:
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Sequence 2, Application US/09858349
Sequence 2, Application US/09858349
Batent No. US20020012909A1
GENERAL INFORMATION:
APPLICANT: PLAKSIN, Daniel
TITE REPERENCE: 87534-2800
CURRENT APPLICATION NUMBER: US/09/858,349
CURRENT FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
SEQ ID NO 2.
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APPLICANT: HAEUW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REFERENCE: 01753-183
CURRENT APPLICATION NOWBER: US/10/735,916A
CURRENT FILING DATE: 2003-12-16
FRIOR PELICATION NUMBER: R03/08 538
FRIOR PELICATION NUMBER: PCT/FR 03/00 178
FRIOR PILING DATE: 2003-07-11
FRIOR PILING DATE: 2003-01-18
FRIOR PILING DATE: 2002-01-18
FRIOR PELING DATE: 2002-01-18
FRIOR PILING DATE: 2002-01-18
FRIOR FILING DATE: 2002-01-18
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TYPE: PRT
ORGANISM: mouse hybridoma specific for H-2D + RGPGRAFVTI peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 85.04
Matches 102; Conservative
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ORGANISM: Homo sapiens
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, ORGANISM: Homo sapiens
US-10-735-916A-81
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   TYPE: PRT
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                                                                                   GENERAL INFORMATION:

APPLICANT: GOETSCH, Liliane
APPLICANT: COCVALA, Nathalie
APPLICANT: DEGER, Olivier
APPLICANT: DEGER, Olivier
APPLICANT: DUFLOS, Alain
APPLICANT: DUFLOS, Alain
APPLICANT: HAEUW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-183
CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT APPLICATION NUMBER: PC7/FR 03/00 538
PRIOR APPLICATION NUMBER: PC0/FR 03/00 178
PRIOR PILING DATE: 2003-01-10
PRIOR APPLICATION NUMBER: FR 02/00 653
PRIOR APPLICATION NUMBER: FR 02/00 654
PRIOR PELING DATE: 2002-01-18
PRIOR PELING DATE: 2002-01-18
PRIOR PELING DATE: 2002-01-18
PRIOR PELING DATE: 2002-05-07
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PATENTIN VOIT: 2.1
SEQ ID NO 79
LENGTH: 117
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### FUDILICANT: GORVAIA, Nathalie
### PEPLICANT: GORVAIA, Nathalie
### APPLICANT: GORVAIA, Nathalie
### APPLICANT: BEGER, Olivier
### APPLICANT: BEGER, Alain
### APPLICANT: BECK, Alain
### APPLICANT: BECK, Alain
### APPLICANT: BECK, Alain
### APPLICANT: HAEUW, Jean-Prancois
### ITILE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
### TILE OF INVENTION: NOWBER: US/10/735,916A
### CURRENT APPLICATION NUMBER: US/10/735,916A
### CURRENT FILING DATE: 2003-01-16
### PRIOR PILING DATE: 2003-01-20
### PRIOR PILING DATE: 2002-01-18
### PRIOR FILING DATE: 2002-01-18
### PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

85.1%; Score 541; DB 5;
Best Local Similarity 84.5%; Pred. No. 2.7e-42;
Matches 98; Conservative 10; Mismatches 8
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Sequence 79, Application US/10735916A
Publication No. US20050084906A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , ORGANISM: Homo sapiens
US-10-735-916A-79
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61 KPSLKDRISITRDTSKNQPPLKLNSVTNEDTATYYCAR-YGRV--PFDYWGQGTTLTVSS 117
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                                                                                                                    2 VOLQESGPGLVXPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNYK
                                                                                                                                                                                                                                     62 PSLKDRISITRDTSKNQFFLKLNSVTNEDTATYYCARYGRVFFDYWGQGTTLTVSS 117
                                                                                                                                                                                                                                                                    1 DVQLQESGPGLVXPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY
                                                             Gaps
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Sequence 83, Application US/10735916A

Publication No. US20050084906A1

GENERAL INFORMATION:
APPLICANT: GOETSCH, Liliane
APPLICANT: LEGER, Olivier
APPLICANT: DUFLOS, Alain
APPLICANT: DUFLOS, Alain
APPLICANT: HAEUW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES
CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT PILING DATE: 2003-12-16
PRIOR APPLICATION NUMBER: PCT/FR 03/00 178

PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
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Query Match 85.1%; Score 541; DB 5; Length 135; Best Local Similarity 84.5%; Pred. No. 3.1e-42; Matches 98; Conservative 10; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: LIAME, TONY W.
APPLICANT: LIAME, TONY W.
APPLICANT: LOO, Deryk T.
APPLICANT: XU, Xiaolin
TITLE OF INVENTION: KID3 AND KID3 ANTIBODIES THAT BIND
TITLE OF INVENTION: THERETO
FILE REFERENCE: 415072002700
CURRENT PELLORION NUMBER: US/10/943,640
CURRENT FILING DATE: 2004-09-17
PRIOR APPLICATION NUMBER: US 60/504,441
PRIOR FILING DATE: 2003-09-18
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASELSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      // FEATURE:
// OTHER INFORMATION: Synthetic Construct
US-10-943-640-4
                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 4, Application US/10943640; Publication No. US20050152907A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Mus sp.
US-09-791-551-119
                                                        JS-09-791-551-119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VOLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNYK 61
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Sequence 85, Application US/10735916A

PUDIJICATION No. US20050084906A1

GENERAL INFORMATION:
APPLICANT: GOETSCH, Liliane
APPLICANT: LEGER, Olivier
APPLICANT: DUFLOS, Alain
APPLICANT: BECK, Alain
APPLICANT: HARMATION: WOUSE, ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 83.2%; Score 529; DB 5; Length 135; Best Local Similarity 82.8%; Pred. No. 4e-41; Matches 96; Conservative 11; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                           Query Match 83.2%; Score 529; DB 5; Length 117; Best Local Similarity 82.8%; Pred. No. 3.5e-41; Matches 96; Conservative 11; Mismatches 9; Indels
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CURRENT FILING DATE: 2003-12-16
PRIOR PAPPLICATION NUMBER: R0 03/08 538
PRIOR FILING DATE: 2003-07-11
PRIOR PRILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: FR 02/00 653
PRIOR PILING DATE: 2003-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 02/00 654
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-05-07
NUMBER: PR 02/05 753
NUMBER: PR 02/05 753
SEQ ID NOS: 156
SEQ ID NOS: 156
PRIOR FILING DATE: 2003-01-20
PRIOR APPLICATION NUMBER: FR 02/00 653
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-05-07
PRIOR PRIOR PLING DATE: 2002-05-07
SPRIOR FILING DATE: 2002-05-07
SPRIOR FILING DATE: 2002-05-07
SPRIOR FILING DATE: 2002-05-07
SPRIOR FILING DATE: 2002-05-07
SEQ ID NOS: 156
SEQ ID NOS: 156
SEQ ID NO 83
LENGTH: 117
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US-10-735-916A-85
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ORGANISM: Homo sapiens
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Sequence 2, Application US/10383447

Sequence 2, Application US/10383447

Publication No. US20040096392A1

GENERAL INFORMATION:

APPLICANT: Blaskar, Vinay

APPLICANT: Law, Debbie

APPLICANT: Law, Debbie

APPLICANT: Ramakrishnan, Vanitha

APPLICANT: Antibodies Against Cancer Antigen TMEFF2 and Uses Thereof

FILE REFERENCE: OSSE2.0138 NPUSG00

CURRENT APPLICATION NUMBER: US 60/362,837

FRIOR APPLICATION NUMBER: US 60/362,837

PRIOR PLING DATE: 2002-03-08

PRIOR FILING DATE: 2002-12-27

NUMBER OF SEQ ID NOS: 34

SEQ ID NO 2.

SEQ ID NO 2.

SEQ ID NO 2.
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Sequence 119, Application US/09791551
Publication No. US20030235584A1
Publication No. US20030235584A1
GENERAL INFORMATION:
APPLICANT: KLOETZER, WILLIAM S.
TITLE OF INVENTION: METHOD FOR PREPARING ANTI-MIF ANTIBODIES
FILE REFRERNCE: 037003/077869
CURRENT APPLICATION NUMBER: US/09/791,551
CURRENT PILING DATE: 2001-02-26
PRIOR FILING DATE: 2000-02-28
PRIOR FILING DATE: 2000-03-28
PRIOR FILING DATE: 2000-03-8
PRIOR FILING DATE: 2000-03-8
PRIOR FILING DATE: 2000-03-8
PRIOR FILING DATE: 2000-03-8
SOFTWARE: PATENTING VOTE: 2000-03-18
SOFTWARE: PATENTING VOTE: 2.1
SEQ ID NO 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.0%; Score 521.5; DB 4; Length 120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 82.2%; Score 522.5; DB 3; Length Best Local Similarity 78.2%; Pred. No. 1.7e-40; Matches 97; Conservative 10; Mismatches 10; Indels
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; OTHER INFORMATION: Heavy chain variable region
US-10-383-447-2
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Best Local Similarity 81.7%; Pred. No. 1.8e-40;
Matches 98; Conservative 7; Mismatches 12; Indels 3; Gaps 1;

Qy 1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY 60

Db 1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWSWIRQFPGNKLEWMGFISYDGSNKY 60

Qy 61 KPSLKDRISITRDTSKNQFFLKLNSVTNBDTATYYCA--RYGRVFFDYWGQGTTLTVSS 117

Db 61 NPSLKNRISITRDTSENQFFLKLNSVTNEDTATYYCA--RYGRVFFDYWGQGTTLTVSS 117

Db 61 NPSLKNRISITRDTSENQFFLKLNSVTTEDTATYYCARGLRRGDYSWDYWGQGTSVTVSS 120
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Search completed: January 10, 2006, 21:35:32 Job time: 65.1754 secs

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2 VQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNYK
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US-09-065-059-11
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                                                                                                                                                             January 10, 2006, 20:34:27; Search time 22.847 Seconds (without alignments) 423.384 Million cell updates/sec
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636
1 DVQLQESGPGLVKPSQSLSL.....RYGRVPFDYWGQGTTLITVSS 117
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Sequence 18,
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/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
/cgn2_6/ptodata/1/iaa/FCOMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
5.1.6
Compugen Ltd
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US-09-925-179-3
US-08-902-486-13
US-08-902-486-15
US-08-466-151-5
US-08-466-163B-5
US-09-802-096-5
US-09-925-179-5
US-07-956-399-2
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US-09-920-171-2
US-09-920-171-2
US-09-716-028-2
US-10-113-996-2
US-08-466-151-3
US-08-466-1538-3
US-09-802-096-3
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US-08-137-117D-31
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GenCore version (c) 1993 - 2006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                               - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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Sequence 100, App
Sequence 101, App
Sequence 10, Appl
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2, Appl
32, Appl
14, Appl
16, Appl
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10, Appl
10, Appl
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APPLICANT: SEINO, Ken-ichiro
APPLICANT: STATA, Hideo
APPLICANT: YAGITA, Hideo
APPLICANT: VAGITA, Hideo
APPLICANT: OKUWURA, Ko
APPLICANT: OKUWURA, Motomi
TITLE OF INVARIA, MOTOMI
TITLE OF INVENTION: THERAPEUTIC AGENT FOR HEPATITIS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCDETMOCK, Will & Emery
STREET: 99 Canal Center Plaza
CITRE: Virginia
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: usa
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,059
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: BUCCA Ph.D., Daniel
REFERENCE/DOCKET NUMBER: P-42,368
REFERENCE/DOCKET NUMBER: P-42,368
REFERENCE/DOCKET NUMBER: 50356-151
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
were
US-08-436-717-31

US-08-466-151-7

US-09-466-153-7

US-09-802-096-7

US-09-922-179-7

US-09-214-095D-13

US-09-214-095D-13

US-09-214-095D-13

US-09-346-114

US-09-345-114

US-09-345-114

US-08-672-345C-10

US-08-672-345C-10
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USA

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ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 6111079west Center, 90 South Seventh St
CITY: Minneapolis
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
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                                                                                                                                                                                                                                                                                                   APPLICANT: KAYAGAKI, No. 6946255uhiko
APPLICANT: YAGITA, Kideo
APPLICANT: YAGITA, Ko
APPLICANT: NCHMORA, Ko
TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFICALLY
TITLE OF INVENTION: REACTING WITH FAS LIGAND AND PRODUCTION PROCESS THEREOF
1 VOLOESGPGLVKPSQSLSLTCSVTGYSITSGYYWNWIRQFPGNKLEWMGYISYDGSNNYN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNYK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VQLQESGPGLVKPSQSLSLTCSVTGYSITSGYYWNWIRQPPGNKLEWMGYISYDGSNNYN 60
                                               62 PSLKDRISITRDTSKNQFPLKLNSVTNEDTATYYCA--RYGRVFFDYWGQGTTLTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PSLKNRISITRDISKNOFFLKLNSVTTEDTATYYCAVYYYDGSSFDYWGQGTTVTVSS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 PSLKDRISITRDTSKNQFFLKLNSVTNEDTATYYCA--RYGRVFFDYWGQGTTLTVSS 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,555
FLING DATE: 19-SEP-1997
CLASSIPICATION: 530
ATTORNEY AGENT INFORMATION:
NAME: Bucca Ph.D., Daniel
REGISTRATION NUMBER: 42,3666,160
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEB: McDermott, Will & Emery
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50356-150
                                                                                                                                                                                                                         Sequence 11, Application US/08913555
Patent No. 6946255
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 5035
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-756-8600
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 118 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
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Sequence 2, Application US/08887352B
Sequence 2, Application US/08887352B
Patent No. 5994511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 KPSLKDRISITRDISKNOPFLKLANSVTNEDTATYYCARYGRV--FFDYWGQGTTLTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAMNMIRQFPGNKLEWMGYISYSGSTSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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84.9%; Score 540; DB 2; Length 119;
Best Local Similarity 84.9%; Pred. No. 1e-49;
Matches 101; Conservative 5; Mismatches 11; Indels
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: Diskette
SOFTWARE: Fatesto Version 1.5
CURSENTANE: DATE
APPLICATION NUMBER: US/08/767,128
FILING DATE: 04-DEC-1996
CLASSIFFCATION NUMBER: PCT/US96/09258
FILING DATE: 05-JUN-1996
FILING DATE: 05-JUN-1995
FILING DATE: 10-OCT-1995
FILING DATE: 10-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: CAFLET, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.49USF1
RELING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: CAFLET, CHARLES
REFERENCE/DOCKET NUMBER: 8648.49USF1
REERSENCE/DOCKET NUMBER: 8648.49USF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 612/332-9081
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ORIGINAL SOURCE:
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US-08-887-352B-2
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Sequence 18, Application US/08767128
Patent No. 6111079
GENERAL INFORMATION:
APPLICANT: WYLIE, DWANE E.
APPLICANT: LOPEZ, OSVALDO
APPLICANT: WIRRAY, PETER JOSEPH
APPLICANT: GOEBEL, PETER

RESULT 3 US-08-767-128-18

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Sequence 2, Application US/09296005

Patent No. 6290957

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

FILE REPERENCE: P1123CIr

FILE REFERENCE: P1123CIr

CURRENT PELLING DATE: 1999-04-21

EARLIER APPLICATION NUMBER: US 08/887,352

EARLIER APPLICATION NUMBER: US 08/887,352

NUMBER OF SEQ ID NOS: 26

SEQ ID NO 2
                                                                  61 KPSLKDRISITRDISKNQFFLKLNSVTNEDTATYYCAR----YGRVFFDYWGQGTTLTVS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 NPSLKARISVTRDTSQNQFFLKLNSATAEDTATYYCARGSHYFGHWHFAVWGAGTTVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DVQLQESGPGLVKPSQSLSLACSVTGYSTTSGYSWNWIRQFPGNKLEWMGSITYDGSSNY 60
  1 DVQLQESGPGLVKPSGSLSLACSVTGYSITSGYSWNWIRQFPGNKLEWMGSITYDGSSNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lowman, Henry B.
APPLICANT: Downan, Henry B.
APPLICANT: Downan, Paula M.
APPLICANT: Jardieu, Paula M.
APPLICANT: Lowe, John Baula M.
APPLICANT: Lowe, John Baula M.
TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
FILE REFERENCE: P1123C2US
CURRENT APPLICATION NUMBER: US/09/920,171
CURRENT FILING DATE: 2001-08-01
FRIOR APPLICATION NUMBER: US 08/887,352
FRIOR APPLICATION NUMBER: US 09/296,005
FRIOR APPLICATION NUMBER: US 09/296,005
FRIOR APPLICATION NUMBER: US 09/296,005
FRIOR PILING DATE: 1999-04-21
NUMBER OF SEQ ID NOS: 44
SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 511; DB 2; Length 121; Pred. No. 1.2e-46; 8; Mismatches 13; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 79.3
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Mus musculus
US-09-296-005-2
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ORGANISM: Mus
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Patent No. 6172213
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe;
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide;
FILE REFERENCE: P1123R1
CURRENT APPLICATION NUMBER: US/09/109,207C
CURRENT FILING DATE: 1998-06-30;
PRIOR FILING DATE: 1997-07-03
NUMBER: OF SEQ ID NOS: 44
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Pred. No. 1.2e-46;
8; Mismatches 13; Indels
                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winbatin (Genentech) CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/887,352B FILING DATE: 03-Jul-1997 CLASSIFICATION: 530
ATTOMENY/AGENT INFORMATION: NAME: Svoboda, Craig G. ATTOMENY/AGENT INFORMATION: NAME: Svoboda, Craig G. REGISTRATION NUMBER: P1123 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION OF SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
TITLE OF INVENTION: Improving Polypeptides NUMBER OF SEQUENCES: 26 CORRESPONDERS ADDRESS: ADDRESSE: Genentech, Inc. STREET: 1 DNA Way CITY: SOUTH San Francisco STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 79.3%;
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LENGTH: 121 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-2
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Best Local Similarity 79.34
Matches 96; Conservative
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LENGTH: 121
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61 KPSLKDRISITRDTSKNQFFLKLNSVTNEDTATYYCAR----YGRVFFDYWGQGTTLTVS 116
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                                                                                                                                                         Score 511; DB 2; Length 121;
Pred. No. 1.2e-46;
8; Mismatches 13; Indels
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APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSES: Genentech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/405617
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185899
FILING DATE: 26-JAN-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAPELICATION NUMBER: 07/879495
FILING DATE: 07-MAY-1992
PRICH APPLICATION DATA:
APPLICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G
NAME: Svoboda, Craig G
NAME: SVOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/466163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08466151
Patent No. 6037453
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TELEPHONE: 650/225-1489
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1 Similarity 79.3%;
96; Conservative 8
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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    NUMBER OF SEQ ID NOS: 44
                                                                       ; TYPE: PRT
; ORGANISM: Mus musculus
US-10-113-996-2
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Best Local Similarity
Matches 96; Conserv
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                          SEQ ID NO 2
LENGTH: 121
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US-08-466-151-3
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Sequence v8-v2
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Sequence v8-v2
Sequence v8-v2
Datent No. 672833
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANTION:
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
FILE REFERENCE: P11231
CURRENT PAPLICATION NUMBER: US/09/116,028
CURRENT FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: US 60/109,207
PRIOR PILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
SEQ ID NO S
SEQ ID NO S
LENGTH: 121
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                                                                                                                                                                61 KPSLKDRISITRDTSKNOFFLKLNSVTNBDTATYYCAR----YGRVFFDYWGQGTTLTVS 116
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                                                                                                                   1 DVQLQESGPGLVKPSQSLSLACSVTGYSITSGYSWNWIRQFPGNKLEWMGSITYDGSSNY 60
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                              4; Gaps
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  79.3%; Pred. No. 1.2e-46;
tive 8; Mismatches 13; Indels
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APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
APPLICANT: Lowe, John
TITLE OF INVENTION: Improved Anti-IgE Antibodies
FILE REFERENCE: P1123C3US
CURRENT APPLICATION NUMBER: US/10/113,996
CURRENT APPLICATION NUMBER: US 08/887,352
PRIOR PELING DATE: 1997-07-02
PRIOR PILING DATE: 1997-07-02
PRIOR APPLICATION NUMBER: US 09/296,005
PRIOR PELING DATE: 1999-04-21
PRIOR PELING DATE: 1999-04-21
PRIOR PELING DATE: 2001-08-01
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Patent No. 6761889
GENERAL INFORMATION:
APPLICANT: Lowman, Henry B.
Best Local Similarity 79.34
Matches 96; Conservative
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; ORGANISM: Mus musculus
US-09-716-028-2
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US-10-113-996-2
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61 KPSLKDRISITRDTSKNOPPLKLNSVTNEDTATYYCAR----YGRVPFDYWGQGTTLTVS 116
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APPLICANT: Jardieu, Paula M.
APPLICANT: Dresta, Leonard G.
TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
FILE REFERENCE: P0718P2C2US
CURRENT APPLICATION NUMBER: US/09/802,077
CURRENT FILING DATE: 1996-03-15
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR PILING DATE: 1994-01-26
PRIOR PLING DATE: 1992-08-14
PRIOR PLING DATE: 1992-08-14
PRIOR PPLICATION NUMBER: US 07/879,495
PRIOR PPLICATION NUMBER: US 07/879,495
PRIOR PLING DATE: 1992-08-14
PRIOR PLING DATE: 1992-08-14
PRIOR PLING DATE: 1991-08-14
SHOR PILING DATE: 1991-08-14
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79.3%; Pred. No. 1.4e-46;
iive 8; Mismatches 13;
CURRENT APPLICATION NUMBER: US/09/802,096
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR PILLING DATE: 1995-03-15
PRIOR FILLING DATE: 1995-03-15
PRIOR PLILNG DATE: 1994-01-26
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR APPLICATION NUMBER: PCT/US92/06860
PRIOR APPLICATION NUMBER: US 07/899,495
PRIOR PLILNG DATE: 1992-05-07
PRIOR PLILNG DATE: 1992-05-07
PRIOR PLILNG DATE: 1991-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 3, Application US/09802077; Patent No. 6699472; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 79.3
Matches 96; Conservative
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Best Local Similarity 79.3
Matches 96; Conservative
                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 64
SEQ ID NO 3
LENGTH: 134
                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Mus musculus
US-09-802-096-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Mus musculus
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US-09-802-077-3
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Patent No. 6685939
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended FILE REPERBNCE: P071892C3US
                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                    61 KPSLKDRISITRDTSKNQFFLKLNSVTNEDTATYYCAR----YGRVFFDYWGQGTTLTVS 116
                                                                                                                                                                                                                                                                                                                                61 NPSLKNRISVTRDTSQNQFFLKLINSATAEDTATYYCARGSHYFGHWHFAVWGAGTTVTVS 120
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                                                                                                       Length 134;
                                                                                                       80.3%; Score 511; DB 2; Length 13·79.3%; Pred. No. 1.4e-46; ive 8; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Dresta, Leonard G.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0718P2C1D1
CURRENT APPLICATION NUMBER: US/08/466,163B
CURRENT FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR PILING DATE: 1995-03-15
PRIOR PILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1992-06-07
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08466163B
Patent No. 6329509
                                                                                                  Query Match
Best Local Similarity 79.31
Matches 96; Conservative
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            Amino Acid
                                   ; TOPOLOGY: Linear
US-08-466-151-3
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US-08-466-163B-3
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61 KPSLKDRISITRDISKNOFFLKLNSVINEDTATYYCAR----YGRVFFDYWGQGTTLTVS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 NPSLKONRISVTRDTSQNQPFLKLNSATAEDTATYYCARGSHYPGHWHFAVWGAGTTVTVS 120
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APPLICANT: Russel, David R.

APPLICANT: Russel, David R.

APPLICANT: Fuller, James T.

TITLE OF INVENTION: METHOD FOR PRODUCING ANTIBODIES AND TITLE OF INVENTION: PROTEIN TOXINS IN PLANT CELLS NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: ADDRESS:

ADDRESSEE: Quarles & Brady

STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                            GENERAL INPORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Preset, Leonard G.
TITLE OF INVENTION: Anti-1gE Antibodies (as amended)
TITLE REFERENCE: P0718P2CIDICIUS
CURRENT APPLICATION NUMBER: US/09/925,179
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 08/466,163
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1995-03-15
PRIOR FILING DATE: 1995-03-15
PRIOR FILING DATE: 1995-03-16
PRIOR FILING DATE: 1995-03-17
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR PILING DATE: 1992-06-07
PRIOR FILING DATE: 1991-08-14
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 68
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US-00-902-486-13
Sequence 13, Application US/08902486
Patent No. 6140075
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Patent No. 6914129
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ZIP: 53701-2113
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-925-179-3
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CITY: Madison
STATE: WI
                                                                         $ 117
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Search completed: January 10, 2006, 20:58:04 Job time: 23.847 secs

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(without alignments)
636.505 Million cell updates/sec
                                                                                            January 10, 2006, 20:07:41 ; Search time 80.7649 Seconds
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1 DVQLQESGPGLVKPSQSLSL......RYGRVFFDYWGQGTTLTVSS
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GenCore version 5.1.6 (c) 1993 - 2006 Compugen Ltd.
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seq length: 200000000
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Perfect score:
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Maximum DB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:\* geneseqp2005s:\*

					SUMMARIES	
Result		Query				
No.	Score	Match	Match Length	8	Ωī	Description
-	636	100.0	117	7	ADJ76903	Adj76903 Anti-IGF
7	636	100.0	117	σ	ADZ67073	Adz67073 Murine i
٣	636	100.0	127	7	ADJ76886	Adj76886 Anti-IGF
4	636	100.0	127	6	ADZ67056	
S	569.5	89.5	118	7	ADJ76904	Adj76904 Anti-IGF
9	569.5	89.5	118	σ	ADZ67074	Adz67074 Mouse an
7	550	86.5	118	~	AAW00829	Aaw00829 Variable
80	550	86.5	118	~	AAW19015	Aaw19015 Anti-hum
6	549	86.3	114	σ	AEA40137	Aea40137 TNF resi
10	548.5	86.2	118	7	ABR82776	Abr82776 Hybridom
11	548.5	86.2	118	7	ABR82886	
12	546	82.8	117	7	ADJ76909	Adj76909 Anti-IGF
13	546	85.8	117	0	ADZ67079	_
14	546	85.8	119	9	ABB98905	Abb98905 Variable
15	546	85.8	135	7	ADJ76911	Adj76911 Anti-IGF
16	546	82.8	135	σ	ADZ67081	1 Human
17	544.5	85.6	136	ᠬ	AAY94391	
18	542	85.2	119	9	ABB98906	
19	541.5	85.1	369	4	AAB73388	Aab73388 Anti-VHS
20	541	85.1	117	7	ADB97814	4
21	541	85.1	117	-	ADJ76913	m
22	541	85.1	117	σ	ADZ67083	m
23	541	85.1	135	7	ADJ76915	Adj76915 Anti-IGF
24	541	85.1	135	σ	ADZ67085	Adz67085 Human an

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	Adg32325 Mouse scF	Adg32362 Precursor	Adg32340 Fusion pr	_	Abb98908 Variable	Adz45405 Murine fa	Ady91369 Anti-KID3	_	Adz51254 Amino aci	Adz42128 Mouse ant		_		Adj76917 Anti-IGF-	Adz67087 Human ant	Adj76919 Anti-IGF-	Adz67089 Human ant	Adt89035 Murine pl	Aea40153 Mouse Igh	Adz81874 Anti-lami
AAW01584	ADG32325	ADG32362	ADG32340	AEC20775	ABB98908	AD245405	ADY91369	ADZ45341	ADZ51254	ADZ42128	ADT07572	ADT07627	ADT07628	ADJ76917	ADZ67087	ADJ76919	ADZ67089	ADT89035	AEA40153	ADZ81874
19 2	-	171 7		322 9	_	119 9	468 9	16 9	116 9	116 9	118 8	_	244 8	117 7	117 9	135 7	135 9	116 8	114 9	118 9
84.9							83.9												82.7	
540	539.5	539.5	539.5	538	536	533.5	533.5	532	532	532	531.5	531.5	531.5	529	529	529	529	527.5	526	524.5
25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; BGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region; CDR. New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers. cytostatic; antipsoriatic; antibody; (FABR ) FABRE MEDICAMENT SA PIERRE. ADJ76903 standard; protein; 117 AA Leger O; Anti-IGF-1R related protein #16. 18-JAN-2002; 2002FR-0000653. 18-JAN-2002; 2002FR-0000654. 07-MAY-2002; 2002FR-0005753. 20-JAN-2003; 2003WO-FR000178 (first entry) Corvaia N, WPI; 2003-569653/53. WO2003059951-A2 Homo sapiens. 06-MAY-2004 24-JUL-2003 Goetsch L, ADJ76903; ADJ76903 

Disclosure; SEQ ID NO 69; 164pp; French.

The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of

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           transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; brasst tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; darmatological disease; immune disorder; immunoglobulin; heavy chain variable region.
                                                                                                                                                                                                                                                     1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murine immunoglobulin heavy chain variable region 7C10 VH SEQ ID NO:69.
                                                                                                                                                                                                                                                                                      61 KPSLKDRISITRDTSKNQPFLKLNSVTNEDTATYYCARYGRVFFDYWGQGTTLTVSS 117
                                                                                                                                                                                                                                                                                                      KPSLKDRISITRDISKNOFFLKLNSVTNEDTATYYCARYGRVFFDYWGGGTTLIVSS 117
                                                                                                                                                                                                                         1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY
                                                                                                                                                                                          Gaps
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                                                                                                                                                          Length 117;
receptors with their ligands. Especially they inhibit
                                                                                            protein sequence used to generate the Ab of the invention.
                                                                                                                                                                                          0; Indels
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                                                                                                                                                         Score 636; DB 7;
Pred. No. 1.2e-51;
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                                                                                                                                                                                        Mismatches
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20-JAN-2003; 2003WO-FR000178.
11-JUL-2003; 2003FR-00008538.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                        Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goetsch L, Corvaia N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2005-321968/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treating
                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GOETSCH L.
CORVAIA N.
LEGER O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DUFLOS A.
                                                                                                                           Sequence 117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US2005084906-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAEUW J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BECK A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-APR-2005.
                                                                                                                                                                                                                                                                                                                                                                                                                                  ADZ67073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DUFL/)
(HAEU/)
(BECK/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CORV/)
(LEGE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GOET/)
                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
ឧដ្ឋមន្ត្រ
                                                                                                                                                                                                                                                  요
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The inversion fracters to a novel isolated anti-insulinity being capable of binding to human IGF-IR and, if necessary, capable of capable of binding to human IGF-IR and, if necessary, capable of capable of binding tromaine kinase activity of the receptor, capable of capable of himbiting tyrosine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acida (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or connected with a definition of the transduction pathway of the signal mediated by the interaction of IGF-IR and/or EGFR, and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly induced to inhibit the transformation of normal cells into cells with tumoral construct, preferably IGF-dependent, especially IGF1 and/or IGF2-dependent and/or EGF-dependent and/or EGF-dependent and/or IGF2-dependent and/or IGF2-dependent
  invention relates to a novel isolated anti-insulin-like growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of IGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGI R and/or EGFR receptor is suspected, which involves contacting the biological sample with (I), which is optionally labeled. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KPSLKDRISITRDTSKNOFFLKLNSVTNEDTATYYCARYGRVFFDYWGQGTTLTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KPSLKDRISITRDTSKNOPFLKLNSVTNEDTATYYCARYGRVFFDYWGQGTTLTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DVQLQESGPGLVKPSQSLSLTCSVTGYS1TGGYLWNWIRQFPGNKLEWMGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 636; DB 9;
100.0%; Pred. No. 1.2e-51;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antipsoriatic; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADJ76886 standard; protein; 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-IGF-1R related protein #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003059951-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADJ76886;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; immunoglobulin; heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 KPSLKDRISITRDTSKNQFFLKLNSVTNEDTATYYCARYGRVFFDYMGQGTTLTVSS 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                   New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 636; DB 7; Length 127; 100.0%; Pred. No. 1.3e-51; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein sequence used to generate the Ab of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 52; 164pp; French
                                                                                                                                                                                                                 (FABR ) FABRE MEDICAMENT SA PIERRE.
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                                                                    18-JAN-2002; 2002FR-0000653.
18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WO-FR000178.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
1es 117; Conservative
                                                                                                                                                                                                                                                                                      Corvaia N,
                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-569653/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 127 AA;
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                                                                                                                                                                                                                                                                                          Goetsch L,
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Matches
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The invention relates to a novel isolated anti-insulin-like growth factor

I receptor (IGF-IR) antibody (I) or its functional fragment, being
capable of binding to human IGF-IR and, if necessary, capable of
capable of binding to human IGF-IR and, if necessary, capable of
capable of binding to human IGF-IR and, if necessary, capable of
comprising a light or heavy chain having at least one complementary
comprising a light or heavy chain having at least one complementary
determining region (CRR) consisting of one of two fully defined 16 amino
control of ADZ67014). An antibody of the invention is useful in
the preparation of a medicament intended for the prevention or treatment
of an illness connected with an overexpression and/or an abnormal
activation of the IGF-IR and/or EGFR, and/or connected with a
hyperactivation of the transduction pathway of the signal mediated by the
cutivation of IGF-IR and/or EGFR, and/or of EGFR, with EGFR;
the administration of the medicament does not induce or only slightly
induces secondary effects connected with inhibition of the insulin
considering the antibody is useful for preparation of a medicament intended
control into and/or IGF-dependent and/or EGFR and/or IGF2-
capendent and/or EGF-dependent and/or HER2/dependent and/or HER2/dependent and/or HER2/dependent and/or HER2-dependent and/or HER2-dependent and/or IGF2-dependent and/or HER2-dependent and/or HER2-dependent and/or IGF2-dependent and/o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (1), which is optionally labeled. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leger O, Duflos A, Haeuw J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 8; SEQ ID NO 52; 125pp; English.
61. .76
/note= "CDR2"
                                        109. .116
/note= "CDR3"
                                                                                                                                                                                                                                                     18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WO-FR001178.
11-JUL-2003; 2003FR-00008538.
                                                                                                                                                                                         16-DEC-2003; 2003US-00735916
                                                                                                                                                                                                                                   2002FR-00000653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corvaia N,
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                                                                                                                                                                                                                                                                                                                                                              GOETSCH L.
CORVAIA N.
LEGER O.
                                                                                                                                                                                                                                                                                                                                                                                                                            DUFLOS A.
HAEUW J.
BECK A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ADZ67055
                                                                                                        US2005084906-A1
                                                                                                                                                                                                                                   18-JAN-2002;
                                                                                                                                                21-APR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goetsch L,
                                                                                                                                                                                                                                                                                                                                                                                                                                (DUFL/)
(HAEU/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BECK/)
                                                                                                                                                                                                                                                                                                                                                                GOET/)
  Region
                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                          LEGE/
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Sequence 127 AA;

/note= "leader peptide" Location/Qualifiers

Mus musculus.

Peptide Region

/note= "CDR1"

Gaps

1;

Indels

8;

Mismatches

5.

Matches 107; Conservative

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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (1) inhibit natural binding of insulin-like growth actors (IGF)-1 and/or -2; and/or (11) inhibit specifically tyrosaine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with heir ligands. Especially they inhibit activity of these receptors with their ligands. Especially they inhibit account of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also orsted for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
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                                                                                                       70
                                                                                                                                                                                                                                                                                                                                                                                                                              insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                             KPSLKDRISITRDISKNQFFLKLNSVTNEDTATYYCARYGRVFFDYWGQGTTLTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                      DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY
                                                                                          Gaps
                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 118;
   Length 127;
                                   Indels
Score 636; DB 9;
Pred. No. 1.3e-51;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 569.5; DB 7
Pred. No. 1.9e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 70; 164pp; French
                                                                                                                                                                                                                                                                                                                                                                                                               cytostatic; antipsoriatic; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (FABR ) FABRE MEDICAMENT SA PIERRE
                                                                                                                                                                                                                                                                    ADJ76904 standard; protein; 118 AA
                                                                                                                                                                                                                                                                                                                                                                              Anti-IGF-1R related protein #17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leger 0;
 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JAN-2002; 2002FR-00000653.
18-JAN-2002; 2002FR-0000654.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-MAY-2002; 2002FR-00005753.
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                                                                                                                                                                                                                                                                                                                                         (first entry)
                  Best Local Similarity 100.
Matches 117; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 118 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus.
                                                                                                                                                                                                                                                                                                                                           06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-JUL-2003.
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                                                                                                                                          61
 Query Match
                                                                                                                                                                                                                                   RESULT 5
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The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of expecifically inhibiting tyrosine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal appearativation of the IGF-IR and/or connected with a nyereactivation of the IGF-IR and/or connected with a interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where
                                                                                                                                                                                                                                                                                                                                                    neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
                                                                                      61 NPSLKORISITRDISKNOPFLKLNSVITEDIATYYCAREGYGYFFDYWGQGTTLITVSS 118
                                                                 61 KPSLKDRISITRDTSKNQFFLKLNSVTNEDTATYYCARYG-RVFFDYWGQGTTLTVSS 117
                                  1 DVÓLÓESGPGLVKPSÓSLSLTCSVTGYSITSGYYWNWIRQFPGNKLEWMGYINYDGNNNY
1 DVQLQESGPGLVXPSQSLSLTCSVTCYSITGGYLWNWIRQFPGNXLEWMGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                      Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beck
                                                                                                                                                                                                                                                                                                     Mouse antibody heavy chain variable region SEQ ID NO:70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haeuw J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Duflos A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 13; SEQ ID NO 70; 125pp; English.
                                                                                                                                                                                              Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leger O,
                                                                                                                                                                                            ADZ67074 standard; protein; 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-JAN-2002; 2002FR-0000653.
18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003MO-FR000178.
11-JUL-2003; 2003FR-00008538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-DEC-2003; 2003US-00735916
                                                                                                                                                                                                                                                                                                                                                                                                                                            heavy chain variable region.
                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corvaia N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2005-321968/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GOETSCH L.
CORVAIA N.
LEGER O.
DUFLOS A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAEUW J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2005084906-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BECK A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus.
                                                                                                                                                                                                                                                                  30-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-APR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goetsch L,
                                                                                                                                                                                                                               ADZ67074;
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(HAEU/) I
(BECK/) I
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(LEGE/)
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                                                                                                                                                         RESULT 6
                                                                                                                                                                            ADZ67074
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25; Page 86-87; 133pp; Japanese.

Claim

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the administration of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin receptor. The antibody is useful for preparation of an edicament intended to inhibit the transformation of normal calls into calls with tumoral character, preferably IGP-dependent, especially IGP1 and/or IGP2-dependent and/or HERZ/neu-dependent calls. [I] is useful for preparation of a medicament intended to inhibit the growth and/or the proliferation of tumor calls, preferably IGP-dependent, and/or IGP2-dependent in the preparation of a medicament intended for prevention or for the treatment of cancer, where the cancer is chosen from prostate cancer, osteosarcoma, lung cancer, breast cancer, endometrial cancer or colon cancer. (I) is useful in the preparation of a medicament intended for the prevention or for the preparation of a medicament intended for the prevention or for the intended for the specific targeting of a biologically active compound to calls expressing or overexpressing the IGP-IR and/or EGRR receptor. (I) is useful for in vitro diagnosis of illnesses induced by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      biological sample with (I), which is optionally labeled. The present sequence is used in the exemplification of the invention.
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                                                                                              61 KPSLKDRISITRDISKNQFFLKLNSVTNEDTATYYCARYG-RVFFDYWGQGTTLTVSS 117
                                                           1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY
                         Gaps
                       1;
 Length 118;
                         Indels
  DB 9;
Score 569.5; DB 9;
Pred. No. 1.9e-45;
2; Mismatches 8;
  89.5%;
             Best Local Similarity 90.7
Matches 107; Conservative
   Query Match
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61 NPSLKNRISITRDTSKNOFFLKINSVTTEDTATYYCAREGYGYFFDYMGQGTTLTVSS 118

AAW00829 standard; protein; 118 AA. (first entry) 19-MAY-1997 AAW00829; RESULT 7 AAW00829 

Variable heavy chain of anti-human Fas ligand antibody NOK-4.

Variable region; heavy chain; human; Fas ligand; monoclonal; antibody; NOK-4 hybridoma; inhibition; apoptosis; assay; diagnosis; disease; hepatitis; infectious mononucleosis; systemic lupus erythematosus.

Mus musculus

WO9629350-A1

21-MAR-1996; 26-SEP-1996

95JP-00087420 95JP-00303492 20-MAR-1995;

96WO-JP000734

(SUME ) SUMITOMO ELECTRIC IND CO. 27-OCT-1995;

Nakata Okumura K, Yagita H, Kayagaki N,

WPI; 1996-443140/44. N-PSDB; AAT39555

Monoclonal antibody specifically recognising the Fas ligand - useful for the detection of Fas ligands either on cell surface or in solution.

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The present sequence is the heavy chain variable region of the anti-human Fas ligand monoclonal antibody (MAb) NOK-4. NOK-4 is produced by the hybridoma NOK-4 (FERM BP-5047), which was prepared by immunising mice with transformed human Ras ligand expressing COS cells, and fusing spleen cells isolated from the mice with myeloma P3x63Ag8.653 (ATCC CR1-1580) cells. The MAb recognises the human Fas ligand on the cell surface or in solution, and can be used to inhibit the apoptosis inducing cell surface Fas ligand/Fas reaction. The MAb can also be used for a Fas ligand assay in biological samples (e.g. human blood), especially for disease diagnosis, e.g. hepatitis, infectious mononucleosis and systemic lupus erythematosus
                                                                                                                                                                                                                                                                                                                                  1 VQLQESGPGLVKPSQSLSLTCSVTGYSITSGYYWNWIRQFPGNKLEWMGYISYDGSNNYN 60
                                                                                                                                                                                                                                                                                                              2 VOLQESGPGLVKPSQSLSLTCSVTGYSITGGYLMNWIRQFPGNKLEWMGYISYDGTNNYK 61
                                                                                                                                                                                                                                                                                                                                                                                           62 PSLKDRISITRDISKNOPFLKLNSVINEDTATYYCA -- RYGRVFFDYWGOGTTLTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heavy chain; variable region; mouse; murine; human; Fas ligand; FasL; monoclonal antibody; MAb; hybridoma; treatment; hepatitis; hepatitis B virus; HBV; hepatitis C virus; HCV; apoptosis; liver cell; glutamate oxaloacetate; pyruvate transaminase.
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                  5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-human Fast antibody (NOK4) heavy chain variable region.
                                                                                                                                                                                                                                                 Score 550; DB 2; Length 118; Pred. No. 1.3e-43; 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW19015 standard; protein; 118 AA
                                                                                                                                                                                                                                                    86.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-JAN-1998 (first entry)
                                                                                                                                                                                                                                                                                  Matches 104; Conservative
                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                          Sequence 118 AA;
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Anti-human Fas Ligand antibody to treat hepatitis – controls apoptosis in The present sequence is the heavy chain variable region of the murine anti-human Fas ligand (Fast) monoclonal antibody (MAD) NOK4, which is expressed by the hybridoma NOK4 (FERM BP-5044). The MAD can be used in the preparation of a composition for the effective oral or parenteral treatment of hepatitis, including hepatitis caused by hepatitis B or C virus. The composition controls apoptosis in liver cells caused by the Nakata M; Okumura K, liver cells and improves liver function. Claim 6; Page 36-37; 51pp; Japanese. (SUME ) SUMITOMO ELECTRIC IND CO. Yagita H, 96WO-JP003089 95JP-00303491. Seino K, Kayagaki N, WPI; 1997-258767/23. N-PSDB; AAT69539 24-OCT-1996; 27-OCT-1995; WO9715326-A1 01-MAY-1997. Mus sp.

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RESULT 10
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binding of Fast to Fas expressing liver cells, and improves liver function by improving blood glutamate oxaloacetate and pyruvate transaminase levels. The composition is given in a dosage of 0.0001-1000, preferably 0.01-600 mg/day. Spleen cells from mice immunised with Fast expressing COS cells were fused with mouse myeloma cells to produce hybridomas. The hybridomas were screened for anti-Fast activity, and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a method for preparing variable region genes of high affinity tumor necrosis factor (TMF) resistant monoclonal antibody (F6 mAb). The method comprises using recombinant human TMF immune BALB/c mouse to prepare mouse anti-TMF monoclonal antibody, screening high
                                                                                                                                                                                              61
                                                                                                                                                                                                                       1 VOLOESGPGLVKPSQSLSLTCSVTGYSITSGYYWWWIRQFPGNKLEWMGYISYDGSNNYN 60
                                                                                                                                                                                                                                                              PSLKDRISITRDISKNQFFLKLNSVTNEDTATYYCA--RYGRVFFDYWGQGTTLTVSS 117
                                                                                                                                                                                            VQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNYK
                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of tumor
                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                                     necrosis factor; TNF; monoclonal antibody; P6 mAb; chain variable region; F6VH.
                                                                                                                                        Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                            TNF resistant monoclonal antibody VH region, F6VH protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Variable region gene of high affinity monoclonal antibody necrosis factor and its preparation.
                                                                                                                                                                 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "CDR3"
/note= "Specifically claimed in Claim 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "Specifically claimed in Claim 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "CDR2"
/note= "Specifically claimed in Claim
                                                                                                                                       Score 550; DB 2;
Pred. No. 1.3e-43;
                                                                                                                                       Query Match
86.5%; Score 550; DE
Best Local Similarity 88.1%; Pred. No. 1.3e
Matches 104; Conservative 3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 2-3; 20pp; Chinese.
                                                                                                                                                                                                                                                                                                                                            AEA40137 standard; protein; 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28. .33
/note= "CDR1"
                                                                                 active clones NOK1-5 isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-NOV-2003; 2003CN-01105919
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                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96. .103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu X, Zhu C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2005-153078/17.
N-PSDB; AEA40136.
                                                                                                                                       Query Match
Best Local Similarity
                                                                                                             Sequence 118 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                   28-JUL-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CN1544466-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-NOV-2004
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                                                                                                                                                                                                                                                                                                                                                                        AEA40137;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
Region
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affinity F6 mAb using an indirect enzyme linked immunosorbent assay (ELISA). By cloning the monoclonal antibody light chain and heavy chain variable region (VI, and VH respectively) genes, the monoclonal antibody light chain and heavy chain variable region gene sequence and amino acid sequence can be obtained, and the unicity of the gene sequence and protein sequence can be confirmed. This sequence represents the amino
                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                           63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD22; B-cell malignancy; anti-CD22 antibody; cytostatic; human; HB22-33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hybridoma HB22-33 anti-CD22 MAb heavy chain Vh-D-Jh junction sequence.
                                                                                                                                                                                                                                                                           LQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNYKPS
                                                                                                                                                                                                                                                                                                                1 LOESGPGLVKPSQSLSLTCSVSGYSITSGYFWNWIRQFSGNKLEWMGYISYDGSNNYNPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                        LKDRISITRDISKNOPFLKLNSVTNEDTATYYCARYGRVFFDYWGQGTTLTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                             114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treating a human patient diagnosed with a B-cell malignancy by administering a blocking anti-CD22 monoclonal antibody binding first two Ig-like domains of native human CD22 (hCD22).
                                                                                                                                                                                                Length 114;
                                                                                                                                                                                                                                       8; Indels
                                                                                                                                                                                              Score 549; DB 9;
Pred. No. 1.5e-43;
5; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 31; Fig 15; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABR82776 standard; protein; 118
                                                                                                                                                                                                86.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-FEB-2003; 2003WO-US005323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-FEB-2002; 2002US-0359419P.
21-OCT-2002; 2002US-0420472P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-DEC-2003 (first entry)
                                                                                                                                                                                                                                       Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYDU-) UNIV DUKE.
(REGC ) UNIV CALIFORNIA.
                                                                                                                   acid sequence for F6VH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tuscano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-712652/67.
                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ACF36426
                                                                                                                                                            Sequence 114 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-SEP-2003
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treating an autoimmune disease or a B-cell malignancy in a human patient comprises administering an amount of an anti-CD22 monoclonal antibody to the patient and monitoring the response of the disease to the treatment.
                                                                         9
                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                           CD22; autoimmune disease; anti-CD22 antibody; iImmunosuppressive; cytostatic; nephrotropic; dermatological; antiinflammatory; anti-ulcer; antirheumatic; antiarthritic; antipsoriatic; thyromimetic; antianemic; antidiabetic; antiallergic; gene therapy; HB22-33.
                                                                                                                                                            NPSLKORISITRDTSKNOFFLKLNSVTTEDTATYYCARGGITVAMDYWGQGTSVTVSS 118
                                                                                                                                         61 KPSLKDRISITRDISKNOPFLKLMSVTNEDTATYYCARYG-RVPFDYWGQGTTLTVSS 117
                                                                         1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY
                                                                                                        EVOLOESGPGLVKPSQSLSLTCSVTGYSITSGYYWNWIRQPPGNKLEWMGYIRYDGSNNY
                                           Gaps
                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 118;
          Length 118;
                                                                                                                                                                                                                                                                                                                                                              Hybridoma HB22-33 anti-CD22 MAb heavy chain (VH) fragment.
                                         Indels
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Pred. No. 1.8e-43;
5; Mismatches 9;
          Score 548.5; DB 7
Pred. No. 1.8e-43;
86.2%; Scor.
87.3%; Pred. No. 1...
5; Mismatches
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                                                                                                                                                                                                                                                          ABR82886 standard; protein; 118
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21-OCT-2002; 2002US-0420472P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-FEB-2003; 2003WO-US005549.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86.2%;
ilarity 87.3%;
Conservative
                                                                                                                                                                                                                                                                                                                             (first entry)
                                           103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2003-721765/68.
                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYDU-) UNIV DUKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ACF36494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 118 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003072736-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                              18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-SEP-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tedder TF;
                                                                                                                                                                                                                                                                                            ABR82886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
          Query Match
Best Local 8
                                           Matches
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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine (IGF)-1 and/or -2; and/or (iii) inhibit specifically tyrosine (IGF)-1 and/or -2; and/or (iii) inhibit specifically tyrosine (IGF)-1 and/or epidermal growth factor receptor (EGFR) and/or with or opperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit cransformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytostatic; antipsoriatic; antibody; insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                      61 NPSLKNRISITRDTSKNQFFLKLNSVTTEDTATYYCARGGITVAMDYWGQGTSVTVSS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSLKDRISITRDTSKNQFFLKLNSVTNBDTATYYCARYGRVFFDYWGQGTTLTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VOLOESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
61 KPSLKDRISITRDTSKNOFFLKLNSVTNEDTATYYCARYG-RVFFDYWGQGTTLTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.8%; Score 546; DB 7; Length 117; 86.2%; Pred. No. 3e-43; ive 8; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 75; 164pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PABR ) FABRE MEDICAMENT SA PIERRE
                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-IGF-1R related protein #22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leger 0;
                                                                                                                                                                                                                                  ADJ76909 standard; protein; 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JAN-2002; 2002FR-00000653.
18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-JAN-2003; 2003WO-FR000178
                                                                                                                                                                                                                                                                                                                                                                   06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corvaia N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-569653/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2003059951-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goetsch L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N
                                                                                                                                                                                                                                                                                                    ADJ76909;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
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Similarity

Best Local Simi Matches 103;

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9

1 SVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYYWNWIRQFPGNKLEWMGYIRYDGSNNY 60

1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY

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Sequence 117 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JP2002253259-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB98905;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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8466666666666666666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel isolated anti-insulin-like growth factor

I receptor (IGF-IR) antibody (I) or its functional fragment, being
capable of binding to human IGF-IR and, if necessary, capable of
specifically inhibiting tyrosine kinase activity of the receptor,
comprising a light or heavy chain having at least one complementary
comprising a light or heavy chain having at least one complementary
comprising a light or heavy chain having at least one complementary
comprising a light or heavy chain having at least one complementary
comprising a light or heavy chain having at least one created
comprising a light or heavy chain having at least one created
comprising a light or heavy chain having at least one treatment
comprising a light or medicament intended for the prevention of the setul in
comprising a light or IGFP with IGF-IR and/or of EGFP with EGFR, and/or of EGFP, and home
comprising a light of the medicament does not induce or only slightly
compressibly IGF-dependent, especially IGF1 and/or IGF2.
character, preferably IGF-dependent, especially IGF1 and/or IGF2.
cueful for preparation of a medicament intended to inhibit the growth
cueful for preparation of tumor cells, preferably IGF-dependent,
cueful for preparation of tumor cells, preferably IGF-dependent.
                                                                                                                                                                                                                                                                                                                                       neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; maculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
PSLKDRITISRDTSKNOFSLKLSSVTAADTAVYYCARYGRVFFDYWGOGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                   Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
                                                                                                                                                                                                                                                                   Human antibody 7C10 1 heavy chain variable region SEQ ID NO:75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beck A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Duflos A, Haeuw J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 13; SEQ ID NO 75; 125pp; English.
                                                                                                                   ADZ67079 standard; protein; 117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leger O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WO-FR000178.
11-JUL-2003; 2003FR-00006538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-DEC-2003; 2003US-00735916.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2002FR-00000653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful for treating cancer.
                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corvaia N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2005-321968/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GOETSCH L.
CORVAIA N.
LEGER O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DUFLOS A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ь.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo gapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .8-JAN-2002;
                                                                                                                                                                                                                      30-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-APR-2005.
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                                                                                                                                                                      ADZ67079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DUFL/)
(HAEU/)
(BECK/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GOET/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORV/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (LEGE/)
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                                                                      RESULT 13
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                             HERZ/neu-dependent cells. (I) is useful in the preparation of a medicament intended for prevention or for the treatment of cancer, where the cancer is chosen from prostate cancer. (I) is useful in the preparation of a medicament intended for the prevention or for the treatment of psoriasis. (I) is useful in preparation of a medicament intended for the prevention or for the treatment of psoriasis. (I) is useful in preparation of a medicament intended for the specific targeting of a biologically active compound to cells expressing or overexpressing the IGF-IR and/or EGFR receptor is useful for in vitro diagnosis of illnesses induced by an overexpression or an underexpression of the IGF-IR and/or EGFR receptor at any or is useful from a biological sample in which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (I), which is optionally labeled. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene encoding anti-bisphenol A antibody, a recombinant protein and its preparation, a DNA, a vector, a transformant, preparation of a recombinant protein, a kit for determining bisphenol A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VQLQESGPGLVKPSETLSLTCTVSGYSITGGYLWNWIRQPPGKGLEWMGYISYDGTNNYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to sequences for murine heavy chain variable region or light chain variable region of anti-bisphenol A antibody (ABZ21157-ABZ21164 and ABB98905-ABB98912). The sequences are useful for the preparation of recombinant protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VQLQBSGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 PSLKDRISITRDISKNOFFLKLNSVINEDTATYYCARYGRVFFDYWGQGTTLTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Variable region; anti-bisphenol A; antibody; murine; heavy chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 546; DB 9; Length 117;
Pred. No. 3e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85.8%; Score 546; DB 6; Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Variable region anti-bisphenol A antibody chain #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB98905 standard; protein; 119 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 11; 19pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BIOS-) BIO APPLIED SYSTEMS KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.8%;
86.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-MAR-2001; 2001JP-00058673.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-MAR-2001; 2001JP-00058673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-MAR-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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N-PSDB; ABZ21157.
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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF-I and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                         insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                             DVQLQESGPGLVXPSQSLSLTCSVTGYSITGGYLMNWIRQFPGNKLEWMGYISYDGTNNY 60
                                                                                             9
                                                                                                                          61 KPSLKDRISITRDTSKNOFFLKLNSVTNEDTATYYCAR-YGRVF-FDYWGQGTTLTVSS 117
                                                                                                                                            New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                              Gaps
                              .;
3
Disclosure; SEQ ID NO 77; 164pp; French.
                                                                                                                                                                                                                                                                                                                                                                              cytostatic; antipsoriatic; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (FABR ) FABRE MEDICAMENT SA PIERRE.
                                                                                                                                                                                                                                             ADJ76911 standard; protein; 135 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goetsch L, Corvaia N, Leger O;
                                                                                                                                                                                                                                                                                                                                                Anti-IGF-1R related protein #23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JAN-2003; 2003WO-FR000178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JAN-2002; 2002FR-00000653
                                                                                                                                                                                                                                                                                                              (first entry)
                                 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-569653/53.
               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2003059951-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-JUL-2003.
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                                 Matches
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Gaps

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85.8%; Score 546; DB 7; Length 135; 86.2%; Pred. No. 3.5e-43; Live 8; Mismatches 8; Indels

Query Match Best Local Similarity 86.2 Matches 100; Conservative

Search completed: January 10, 2006, 20:44:16 Job time : 81.7649 secs

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OM protein - protein search, using sw model

January 10, 2006, 20:28:02 Run on:

, Search time 14.1157 Seconds (without alignments) 797.508 Million cell updates/sec

US-10-735-916A-69 636 1 DVQLQESGPGLVKPSQSLSL......RYGRVFFDYWGQGTTLIVSS 117 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR\_80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Ig heavy chain V r	heavy		heavy	heavy	heavy	heavy	heavy	heavy	heavy	g heavy chain	heavy		heavy	heavy chain	heavy chain	heavy	heavy	ne C72-3A1 pr	heavy	heavy	heavy	heavy chain				mu cha		Ig heavy chain V r
Others	MAKIES		70																												
200	E S S			AVMS35	E25114	<b>S38718</b>	128195	S07637	C53285	A25114	F25114	PL0100	C25114	830752	T01262	B24672	HVMS31	D25114	S26467	842771	157810	S26464	859639	HVMS1B	G2MS60	S14485	S14484	137782	D33932	44	S14486
		DB	N	~	~	7	~	7	~	~	~	~	N	~	N	~	-	~	~	~	~	~	~	-	-	7	~	~	~	N	7
		Length	121	137	119	116	117	136	119	120	115	135	119	149	114	134	116	119	104	123	117	106	106	116	113	100	101	140	115	102	102
	*		85.7	84.1	82.2	82.0	81.9	81.7	80.2	80.0	79.2	79.2	79.1	79.1	78.5	78.5	78.5	74.8	74.0	72.8	72.6	72.6	71.9			66.8	9.99	66.5	66.4	66.1	64.9
		Score	545	535	523	521.5	521	519.5	510	508.5	504	503.5	503	503	499.5	499.5	499	476	470.5	463	462	461.5	457	455	447	425	423.5	423	422.5	0	413
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	Ig heavy chain pre Ig heavy chain V r Iq heavy chain V r		heavy heavy	heavy heavy	heavy heavy	heavy	heavy heavy	
S31690 S13685	HVMS73 S13686 S14487	S13687 S30530	S31511 S44114	S13519 S42484	S31512 S30534	S13688	S24443 S78052	
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130	117	111	155 129	147	155	110	118	
64.2	63.6 63.4 63.1	62.9	61.8	61.6	60.8 60.6	60.4	60.3	
408	404.5 403 401	400 399	393 392.5	392 388.5	385.5	384	383.5 383.5	
30	u u u u u u u u u	36.3	37	3 6 <b>4</b> 0 0	4 4 2 2	43	<b>4</b> 4 5	

## ALIGNMENTS

RESULT 1 537200 C; Species Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Species: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000 C; Accession: 53720 A; Description: Production and cloning of TMV-specific monoclonal antibodies. A; Reference number: 537200 A; Reference number: 537200 A; Reference number: 537200 A; Reference number: 537200 C; Status: preliminary A; Molecule type: mRNA A; Residues: 1-121 <fis> A; Residues: 1-121 <fis> C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Superfamily: immunoglobulin V region; immunoglobulin homology</fis></fis>
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1; 4; Gaps Query Match 85.7%; Score 545; DB 2; Length 121; Best Local Similarity 86.0%; Pred. No. 5.3e-43; Matches 104; Conservative 3; Mismatches 10; Indels

9 9 1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITSSYYWNWIRQFPGNKLEWMGYISYDGRNDY 1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY a ò

116 61 KPSLKDRISITRDTSKNOFFLKLNSVTNEDTATYYCARYGRV----FPDYWGQGTTLTVS à

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RESULT 2 AVMS35

Avmosts

Ig heavy chain precursor V region (MOPC 315) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 24-Apr-1894 #sequence revision Joun-1992 #text\_change 09-Jul-2004
C;Accession: PL0102; S03262; A93814; A91462; A93787; S23599
R;Rinfret, A.; Horne, C.; Dorrington, K.J.; Klein, M.
Mol. Immunol. 26, 431-434, 1989
A;Title: Cloning, sequencing and expression of the rearranged MOPC 315 VH gene segment.
A;Reference number: PL0102; MUID:89238351; PMID:2497341
A;Reference number: PL0102; MUID:89238351; PMID:2497341
A;Residues: 1-137 cRIN>
A;Residues: 1-137 cRIN>
A;Residues: UNIPROT:P01822; UNIPARC:UP1000002727B; GB:M27638; NID:g602706; PIDN
A;Cross-references: UNIPROT:P01823; UNIPARC:UP1000002727B; GB:M27638; NID:g602706; PIDN
B;Rinfret, A.; Dorrington, K.J.; Klein, M.
SkRinfret, A.; Dorrington, K.J.; Klein, M.
Submitted to the EMBL Data Library, June 1988

germ-lin

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A;Accession: E25114
A;Aolecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-119 <0LiL>
A;Cross-references: UNIPARC:UPI0000115D24; GB:X03378; NID:g52007; PIDN:CAA27095.1; PID:g.
C;Superfeanily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <1MM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPPARC:UP10000117542; EMBL:X76018; NID:g416102; PIDN:CAA53605.1; PI C. Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin momology cIMM> F;15-98/Domain: immunoglobulin homology cIMM>
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A; Residues: 1-117 cSHE>
A; Cross-references: UNIPARC: UP10000114D72; GB:M19775; NID:g195526; PIDN:AAA38343.1; PID
A; Note: the authors translated the codon AAC for residue 61 as Thr, and did not translat
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Superfamily: immunoglobulin homology < IMM>
F;15-98/Domain: immunoglobulin homology < IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä
A,Title: The idiotypic network and the internal image: possible regulation of A,Reference number: A91028; MUID:86136012; PMID:3937730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C;Accession: S38718
R;Cimanis, A.Y.
submitted to the EMBL Data Library, November 1993
A;Accession: S38718
A;Accession: S38718
A;Accession: C;Accession: C;Acces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYYWNWIRQFPGNKLBWMGYISYDGSHNY
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                                                                                                                                                                                                                                                                                                                                                                                                                         Length 119;
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Pred. No. 5.3e-41;
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83.8%; Pred. No. 7.1e-41;
iive 5; Mismatches 13
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                                                                                                                                                                                                                                                                                                                                                                                                                82.2%;
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Matches 99; Conservative
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Matches 98, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig heavy chain V region (HP25) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 20-Jun-2000
C;Accession: E251H *sequence_revision 6.; Theze, J.; Fougereau, M.
EMBO J. 4, 3681-3688, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY
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Them 11; Indels
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84.1%; Score 535; DB
Best Local Similarity 83.2%; Pred. No. 5e-4;
Matches 99; Conservative 7; Mismatches
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E25114
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A;Molecule type: mRNA
A;Residues: 1-120 <OLL>
A;Cross-references: UNIPARC:UP10000115D15; GB:X03374; NID:g51983; PIDN:CAA27071.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: hererotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig heavy chain V region (HP12) - mouse (Species: Mus musculus (house mouse) (Cjspecies: Mus musculus (house mouse) (Cjspecies: Mus musculus) (house mouse) (Cjspecies: Mus musculus) (Ascession: F22114 (Ascession: F22114 (Ascession: F23114 (Ascession: F32114 (As
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                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                         "Ig heavy chain V region (HP22, HP27) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 21-Jul-2000
C;Accession: A25114
R;Ollier, P:; Rocca-Serra, J:; Somme, G.; Theze, J.; Fougereau, M.
B;Ollier, P:; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau, M.
B;MBO J. 4, 3681-3688, 1985
A;Title: The idiotypic network and the internal image: possible regulation of A;Reference number: A91028; MUID:86136012; PMID:3937730
            1 DVQLQESGPGLVKPSQSLSLTCSVTGYSIISGYYWNWIRQFPGDKLEWMGFIRYDGSNNY
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Pred. No. 2.8e-39;
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Ig heavy chain precursor V region (40-140) - mouse
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81.7%; Pred. No. z...
5; Mismatches
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A, Molecule type: mRNA
A, Residues: 1-115 <OLL>
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Matches 95; Conserv
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C53285
Ig heavy chain V and J regions, monoclonal antibody OHP7D7.2.3 - mouse (fragment)
C; Species: Was musculus (house mouse)
C; Date: 02-May-1994 #Sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C; Date: 02-May-1994 #Sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C; Date: 02-May-1994 #Sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C; Accession: C53285
R; Sawada, J; Mizusawa, S.; Terao, T.; Naito, M.; Kurosawa, Y.
Mol. Immunol. 28, 1063-1072, 1991
A; Title: Molecular characterization of monoclonal anti-steroid antibodies: primary struct and their pH-reactivity profiles.
A; Reference number: A53285; MUD:92017897; PMID:1922102
A; Accession: C53285
A; Status: preliminary
A; Molecule type: mRNA; protein
A; Residues: 1-119 < SAW>
A; Cross-references: UNIPARC:UPI000011D0A5; GB:D12734; NID:g220548; PIDN:BAA02226.1; PID: A; Note: sequence extracted from NCBI backbone (NCBIN:63297, NCBIP:63302)
C; Superfamily: Immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 15-98/Domain: immunoglobulin homology < IPMP>
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                         Length 117;
Score 521; DB 2; ......
Pred. No. 8e-41;
Pred. ....hes 14; Indels
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1 Similarity 83.8%; Pred. No. 1.3e-40;
98; Conservative 6; Mismatches 12
                                                                                                          5; Mismatches
                     81.9%;
ilarity 83.8%;
Conservative
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Matches 98; Conserv
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Best Local S
Matches 98
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RESULT 14
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C;Species: Mus musculus (house mouse)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999
C;Accession: PLO100
R;Near, R.I.; Haber, E.
Mol. Immunol. 26, 371-382, 1989
A;Title: Characterization of the heavy and light chain immunoglobulin variable region ge
A;Title: Characterization of the heavy and light chain immunoglobulin variable region ge
A;Accession: PLO100
A;Accession: Use segment is classified as a member of the 36-60 VH gene family
C;Acpertical:
A;Introns: 15/1
C;Auperfamily: immunoglobulin V region; immunoglobulin
C;Acpertical: A;Accession: Segment #status predicted <ARE>
F;11-118/Domain: V segment #status predicted <ARE>
F;11-118/Domain: U segment #status predicted <
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 119;
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Pred. No. 3.6e-39;
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Ig heavy chain precursor V region - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 23-Jul-1999
C;Accession: 530752
R;Grant, F.J; Levin, S.D; Gilbert, T.; Kindsvogel, W.
R) Wicleic Acids Res. 15, 5496, 1987
A;Title: Improved RNA sequencing method to determine immunoglobulin mRNA sequence.
A;Reference number: 530751
A;Accession: 530752
A;Accession: 530752
A;Accession: 530752
A;Residues: 1-149 cGRA-
A;Cross-references: UNIPARC:UPI0000115D92; EMBL:X05878; NID:G52526; PIDN:CAA29302.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;33-116/Domain: immunoglobulin homology <IMM>F;33-116/Domain: c region (C-gamma 2b) (fragment) #status predicted <CRE>
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 21-Jul-2000
C;Accession: T01262
R;Pirofski, L.A.; Thomas, E.K.; Scharff, M.D.
AJDS Res. Hum. Retroviruses 9, 41-49, 1993
A;Title: Variable region gene utilization and mutation in a group of neutralizing murine A;Reference number: Z14285; MUD:93152285; PMID:7678971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gross-references: UNIPARC:UPI0000117638; EMBL:854194; NID:9264864; PIDN:AAB25246.2; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 NPSLKSRISITRDISKNLFFLQLNSVTTEDTATYYCA---RGLDDYWGQGTTLTVSS 114
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Pred. No. 7.2e-39;
6; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.1%; Score 503; DB 2; 79.8%; Pred. No. 4.6e-39; tive 8; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-114 <PIR>
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Best Local Similarity 81.2%;
Matches 95; Conservative (
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Best Local Similarity
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                                                                                                                                                                                                                                                                              Gaps
A;Cross-references: UNIPARC:UPI00001768F5
A;Note: this sequence was determined from the differentiated gene
C;Genetics
C;Genetics
A;Introns: 15/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;19-134/Product: Ig heavy chain V region Vagam3-2 #status predicted <MAT>
P;33-116/Domain: immunoglobulin homology <IMM>
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## RESULT 15 HVMS31

Howay chain precursor V region (M315) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: J70509
R;Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
J. Exp. Med. 169, 2007-2013, 1389
A;Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary in A;Reference number: J7050; MUID:89279149; PMID:2499654
A;Accession: J70509
A;Accession: J70509
A;Reference number: J0501; MUID:89279149; PMID:2499654
A;Accession: J70509
A;Reference: UNIROT:P18531; UNIPARC:UPI00000278E0
A;Residues: 1-116 <LEV>
A;Coss-reference: UNIROT:P18531; UNIPARC:UPI00000278E0
A;Experimental source: strain BALB/cJ
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: signal sequence #status predicted <SIG>
F;1-18/Domain: signal sequence #status predicted <MAT>
F;33-116/Domain: immunoglobulin homology <IMM>

19 DVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYYWNIRQFPGNKLEWMGYISYDGSNNY 78 1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY ö / Match 78.5%; Score 499; DB 1; Length 116; Local Similarity 93.9%; Pred. No. 8.2e-39; nes 92; Conservative 2; Mismatches 4; Indels Matches

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Gaps

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61 KPSLKDRISITRDTSKNOFFLKLNSVTNEDTATYYCAR 98

79 NPSLKANRISITRDTSKNOFFLKLNSVTTEDTATYYCAR 116

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                  GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd
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HV46 MOUSE
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Maximum Match 100%
Listing first 45 summaries
                                                                                           - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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2: uniprot_trembl:*
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seq length: 200000000
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C SISKAINSMIX FUB/N.

C TISSUB-Mammary tumor. WAP-TGF alpha model. 7 months old;

KC TISSUB-Mammary tumor. WAP-TGF alpha model. 7 months old;

KD Straubberg RL.; Feligoold E.A.; Grouse L.H.; Derge J.G.;

KA Stauberg R.L.; Feligoold E.A.; Grouse L.H.; Derge J.G.;

KA Altschul S.F.; Zeeberg B.; Barger L.; Shemmen C.M.; Schuler G.D.;

A Altschul S.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Haich F.;

KA Depkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Haich F.;

KA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;

Raha S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullahy S.J.;

Raha S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullahy S.J.;

Raha S.S.; McGwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;

Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;

Villalon D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;

Rahasley M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;

Rakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;

Rotiguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.;

Butterfield Y.S.N.; Krzywinski M.I.; Skalska U.; Smailus D.E.;

R. Generation and initial analysis of more than 15,000 full-length human
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Bukaryote, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
P01819
O9u175
O9u175
O96331
O96832
O7z374
O8mx3
O99u10
O69mx5
O96aa6
O99ax6
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STRAIN-MAX. PARAL-MAX. PARAL-MAX. PARAL-MAX. PARAL-MAX. PUBL.
STRAIN-MAX. PUB.N.
TISSUE-Mammary tumor. WAP-TGF alpha model. 7 months old;
NIH MGC Project;
NIH MGC Project;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002091; AAH02091.1; -; mRNA.
HSSP; P01820; 1G7J.
CG) GO:0003823; F:antigen binding; IEA.
InterPro; IPR007110; Ig-like.
InterPro; IPR00710; Ig-like.
InterPro; IPR00710; Ig-like.
InterPro; IPR00710; Ig-like.
InterPro; IPR007506; Ig-NG.
INTERPRO; IRR007506; IG-NG.
INTERPRO; IPR007506; IG-NG.
INTERPRO; IRR007506; IG-NG.
INTERPRO; IRR0
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Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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HV43 MOUSE
(9911.75 HUMAN
HV21 HÜMAN
096EYÜ HUMAN
056M842 RAT
(97234 HUMAN
06NYH3 HUMAN
098UX4 HUMAN
096MX5 HUMAN
096AX5 HUMAN
096AX6 HUMAN
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01-07N-2001 (TrEMBLrel. 17,
01-MAR-2004 (TrEMBLrel. 26,
LOC38447 protein.
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Q99M22;
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STRAIN=Mix FVB/N;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-89238351; PubMed=2497341; DOI=10.1016/0161-5890(89)90133-8; Rinfret A., Horne C., Dorrington K.J., Klein M.; "Cloning, sequencing and expression of the rearranged MOPC 315 VH gene
                                                                                                                                                                                                                                                                                        61 KPSLKDRISITRDTSKNOFFLKLANSVTNEDTATYYCARYGRVFFDYWGQGTTLTVSS 117
                                                                                                                                                                                                                                                                                                            1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sclurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                     Gaps
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MEDLINE=79148758; PubMed=428562; Schechter I., Wolf O., Zemell R., Burstein Y.; Structure and function of immunoglobulin genes and precursors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=77244979; PubMed=268248; Hood L., Margolles M.N., Givol D., Zakut R.; Unpublished results, cited by: Unpublished results, cited by: Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.; Cold Spring Harb. Symp. Quant. Bilol. 41:627-637(1977).
-! MISCELLANEOUS: This alpha chain was isolated from a myeloma protein that has anti-dinitrophenyl activity.
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                                                                                                            Length 479;
                                                                                                     Match 85.1%; Score 541; DB 2; Length 47 Local Similarity 85.5%; Pred. No. 1.7e-47; Local 100; Conservative 6; Mismatches 11; Indels
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00299; IG_MHC; UNKNOWN_2.
Immunoglobulin domain.
SEQUENCE 479 AA; 51992 MW; 768E39A138918892 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunoglobulin heavy chain.";
Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696(1977)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
10-MAX-2005 (Rel. 47, Last annotation update)
gheavy chain V region MOPC 315 precursor.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                           137 AA
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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz Fromstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Broak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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                                                                                                                                                                                                                                                                                                                          heavy chain V region MOPC 315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complementarity-determining-3. Framework-4.
By similarity.
G -> GG (in Ref. 1; CAA30727).
G -> H (in Ref. 2).
G -> H (in Ref. 4).
N -> D (in Ref. 4).
Missing (in Ref. 4).
                                                                                                                                                                                                                                                                                                                                                                           Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 137;
                                                                                                                                                                                                                                                                                                                                                                                                                      Complementarity-determining-2.
Framework-3.
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Last annotation update)
                                                                                                                                                                                             SMART; SM00406; IGV; 1.—
PROSITE; PS50835; IG_LIKE; 1..
Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 535; DB 1;
Pred. No. 1.6e-47;
7; Mismatches 11;
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                                                                                                                          musculus
Genomic_DNA
Genomic_DNA
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Framework-1
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                                                                     HSSP, P01820; 1G7J.
SMR; P01822; 20-137.
Ensembl; ENSMUSG0000057048; Mus
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                                                                                                                                            InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
  77
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EMBL; M27638; AAA61337.1;
EMBL; X07880; CAA30727.1;
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QSU413;
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nes 99; Conservative
                                                PL0102; AVMS35.
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 KPSLKDRISITRDTSKNOFFLKLNSVTNEDTATYYCARYGRVF---FDYWGQGTTLTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 DVQLQESGPDLVKPSQSLSLTCTVTGYSITSGYGMHWIRQFPGNKLEWMGXISYSGSNNY 78
Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeeley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=86136012; PubMed=3937730; Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.; Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.; The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic) antibodies in the GAT system."; EMBO J. 4:3681-3688(1985).
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
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                                                                                                                                                                                                                                                                                                                                                                                                                           82.8%; Score 526.5; DB 2; Length ilarity 82.5%; Pred. No. 5.4e-46; Conservative 7; Mismatches 11; Indels
                                                                                                                                                                   NIH MGC Project,
Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, EC085312, AAH85312.1; -; mENA.
Ensembl, ENSMUSG00000054328; Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
EMBL; X03378; CAA27095.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PSS0835; IG LIKE; 4.
PROSITE; PS00290; IG WHC; UNKNOWN 2.
SROHENCE 483 AA; 52714 MW; 7C272DAS01A4A0D1 CRC64;
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13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
VH-D-JH region (Fragment).
                                                                                                and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                            GO; GO:0003823; F:antigen binding; IEA
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                                                                                                                                                                                                                                      InterPro; IPR003599; Ig.
InterPro; IPR00310; Ig-11ke.
InterPro; IPR003109; Ig-21.
InterPro; IPR003006; Ig-MHC.
InterPro; IPR003006; Ig-MHC.
Pfam: PP07654; C1-set; Z.
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Q53VQ5;
13-SEP-2005 (TrEMBLrel. 31,
                                                                                                                                       NUCLEOTIDE SEQUENCE.
STRAIN=FVB/N; TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                             SMART; SM00409; IG; 3.
SMART; SM00407; IGc1; 3.
SMART; SM00406; IGV; 1.
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hes 99; Conserv
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MEDILINE=90067954; PubMed=2587273;

MEDILINE=90067954; PubMed=2587273;

Urakov D.N., Deev S.M., Polyanovsky O.L.;

Urakov D.N., Deev S.M., Polyanovsky D.N.;

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                                                                                                                                                                                                                                                                                                           61 KPSLKDRISITRDTSKNOPFLKLNSVTNEDTATYYCA----RYGRVFF---DYWGQGT 111
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                                                                                                                                                       1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY
                                                                                                                                                                                                   1 DVQLQBSGPGLVKPSQSLSLTCSVTGYSITSGYYWNWIRQFPGNKLEWMGYISYDGSHNY
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
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oglires; Glires; Rodentia; Sciurognathi;
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Score 523; DB 2; Length 11
Pred, No. 2.5e-46;
5; Mismatches 7; Indels
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
VH-D-JH region (Fragment).
Mus musculus (Mouse).
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Last annotation update)
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83.8%; Pred. No. 6.7e-46;
iive 6; Mismatches 12;
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Mammalia, Eutheria, Euarchontoglires,
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       82.2%;
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Q53VR7;
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                                                                                   99; Conservative
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NUCLEOTIDE SEQUENCE.
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                               Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.; "The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic) antibodies in the GAT system.";
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80.0%; Score 508.5; DB 2; Length 120; 79.2%; Pred. No. 8e-45; ive 8; Mismatches 8; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12; Indels
                                                                                                                                                                                                                                                                                              Fougereau M.;
Fougereau M.;
Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databages.
EMBL; X03375; CAA27077.1; -; mRNA.
EMBL; X03374; CAA27071.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fougereau M.;
Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
EMBL; X03379; CAA27101.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 AA; 13892 MW; 013452306EBAA3BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 AA; 13257 MW; D465A5854DF459A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 31, Last sequence update) (TrEMBLrel. 31, Last annotation update)
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81.7%; Pred. No. 2.2e-44;
ive 5; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
MEDLINE=86136012; PubMed=3937730;
                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE OF 28-29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE OF 28-29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-SEP-2005 (TrEMBLrel. 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, VH-D-JH region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q53VQ1_MOUSE PRELIMINARY;
                                                                                                                                                                                      EMBO J. 4:3681-3688(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 79.2
ses 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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MEDLINE=89279149; PubMed=2499654; DOI=10.1084/jem.169.6.2007;
Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
"Early onset of somatic mutation in immunoglobulin VH genes during the
                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
MEDLINE=86136012; PubMed=3937730;
Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
Ollier P., Rocca-Serra d., Somme G., Theze J., Fougereau M.;
The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic) antibodies in the GAT system.";
EMBO J. 4:3681-3688(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DVQLQESGFGLVKPSQSLSLTCSVTGNSITSGYYWSWIRQFPGNKLEWMGYIKYDGNNSY
                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.1%; Score 503; DB 2; Length 119; 79.3%; Pred. No. 3e-44; tive 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fougereau M.;
Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
EMBL; X03376; CAA27083.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 119
119 AA; 13799 MW; 36504D1665BFBB59 CRC64;
                                                                    Last sequence update)
Last annotation update)
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01-NOV-1990 (Rel. 16, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
11g heavy chain V region M315 precursor.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 AA
                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 primary immune response.";
J. Exp. Med. 169:2007-2019(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE OF 28-29.
                                            13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31,
                                                                                                               VH-D-JH region (Fragment).
Q53VR3_MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96; Conservative
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                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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NUCLEOTIDE SEQUENCE.
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MEDLINE-22188257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MELAUSDER R.D., Felngold E.A., Grouse L.H., Derge J.G.,

MAIschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Maltachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Joaden H.B., Bonando M.F., Casavant T.L., Scheetz T.E.,

Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robar S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glibbs R.A.,

Rahesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schwuctz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schwuctz J., Myers R.M.,

Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,

Bronnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Bronnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Bronnerch A., Schein J.E., Mores S.J.M., Marra M.A.;

Bronnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                     Ensembl; ENSMUSG0000057048; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IRR003596; Ig-v.
SMART; SMO0406; IGv; 1.
3PROSTE; PS50835; IG LIKE; 1.
3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.5%; Score 499; DB 1; Length 116; 93.9%; Pred. No. 7.5e-44;
                                                                                                                                                                                                                                                                                                Complementarity-determining-1
                                                                                                                                                                                                                                                                                                                                             Complementarity-determining-2
                                                                                                                                                                                                                                                   chain V region M315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       116 AA; 13095 MW; 4562E03E53DC9E10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 NPSLKNRISITRDTSKNQPFLKLNSVTTEDTATYYCAR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 KPSLKDRISITRDTSKNQFFLKLNSVTNEDTATYYCAR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      590 AA
                                                                                                                                                                                                                                                                                                                                                                                          By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                       Framework-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30,
                                          PDB; 1EZV; X-ray; X=22-116.
SMR; P18531; 19-116.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92; Conservative
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Q569B8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                       JT0509; HVMS31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 92; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxiD=10116;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 KPSLKDRISITRDISKNQFFLKLNSVTNEDTATYYCARYGRVF--FDYWGQGTTLTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLECTIDE SEQUENCE.
MEDLINE=86136012; PubMed=3937730;
Ollier D., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic) antibodies in the GAT system.";
EMBO J. 4:3681-3688(1985).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
%
TISSUE=Spleen,
Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
REBL; BC092580; AAH92580.1; -; mRNA.
GO; GO:0003823; F:anttigen binding; IEA.
RINTERPO; IPR003929; Ig.
RINTERPO; IPR003599; Ig.
RINTERPO; IPR003599; Ig.
RINTERPO; IPR003006; Ig_MHC.
RINTERPO; IPR003906; Ig_MHC.
R SWART; SM00409; IG-1; 4.
R SWART; SM00409; IG-1; 5.
R PROSITE; PS00290; IG-LIKE; 5.
R PROSITE; PS00290; IG-LIKE; 5.
R SEQUENCE 590 AA; G5088 MW; FAC77FFAB2302304 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77.4%; Score 492; DB 2; Length 590; 79.0%; Pred. No. 2.6e-42; ive 7; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fougereau M.;
Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
EMBL; X03378; CAA27096.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98 AA; 11202 MW; 4049CF8C7EE8AAE0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 NPSLKORISITRDTSKNQPFLKLNSVTIEDTATYYCAR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77.2%; Score 491; DB 2;
92.9%; Pred. No. 4.2e-43;
iive 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 KPSLKDRISITRDTSKNOFFLKLNSVTNEDTATYYCAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE OF 28-29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q53VQ4 MOUSE PRELIMINARY;
Q53VQ4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VH region (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Altachul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A. Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rachiguez A., Gunaratne P.H.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodiguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    щ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 KPSLKDRISITRDTSKNQFFLKLNSVTNEDTATYYCAR-----YGRVFFDYWGQGTTLT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 NPSLKSRISITRDISKNQFFLQLNSVTTEDTATYYCARCHGGPLTGR-YFDYWGQGVMVT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.9%; Score 489; DB 2; Length 61
76.4%; Pred. No. 5.7e-42;
ive 10; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases EMBL; BC092582; AAH92582.1; -; mRNA.
GO; GO:0003823; Frantigen binding; IEA.
                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                     615 AA
                                                               Created)
                                     PRT;
                                                           10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, LOC314509 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94; Conservative
                                   Q569B6_RAT PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003599; Ig.
                                                                                                                               Rattus norvegicus (Rat)
                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                              NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Spleen;
NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 VSS 117
                                                                                                                                                                                                                     TISSUE=Spleen
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                                                  Q569B6;
          RESULT 12
Q569B6_RAT
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                       Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.; "The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic) antibodies in the GAT system.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DVHLQESGPGLVKPSQSLSLTCSVTGYSITRGYNWNWIRRFPGNKLEWMGYINYDGSNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=86136012; PubMed=3937730; Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.; Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.; The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic) antibodies in the GAT system."; EMBO J. 4:3681-3688(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLWNWIRQFPGNKLEWMGYISYDGTNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75.5%; Score 480; DB 2; Length 98; 88.8%; Pred. No. 5.8e-42; ive 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fougereau M.;
Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fougereau M.;
Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 AA; 11255 MW; EBC71AA2P8F5FD60 CRC64;
                                                                                                                                                 13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 NPSLKNRISVTRDTSKNQFFLKMNSVTTEDTATYYCAR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 KPSLKDRISITRDTSKNQFFLKLNSVTNEDTATYYCAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 AA
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                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X03375; CAA27078.1; -; mRNA. EMBL; X03374; CAA27072.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=86136012; PubMed=3937730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q53VQ9 MOUSE PRELIMINARY;
Q53VQ9;
13-SEP-2005 (TrEMBLrel. 31, C:
13-SEP-2005 (TrEMBLrel. 31, Li
13-SEP-2005 (TrEMBLrel. 31, Li
VH-D-JH region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE OF 28-29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE OF 28-29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBO J. 4:3681-3688(1985).
                                                                                                          Q53VR6_MOUSE PRELIMINARY;
Q53VR6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                       VH-region (Fragment)
Mus musculus (Mouse)
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
137 VSS 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q53VR2_MOUSE PRELIMINARY; PRT; 98 AA.
053VR2_
053VR2_
13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Whregion (Fragment).
Whr egion (Fragment).
Whis musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Burchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.

NCBI_TAXID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLECTIDE SEQUENCE.
MEDLINE=86136012; PubMed=3937730;
Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
"The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic) antibodies in the GAT system.";
EMBO J. 4:3681-3688(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                              8; Gaps
                                                                                                                                                                                                             ch 74.8%; Score 476; DB 2; Length 119; 1 Similarity 75.4%; Pred. No. 1.9e-41; 89; Conservative 9; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 74.7%; Score 475; DB 2; Length 98 Best Local Similarity 89.8%; Pred. No. 1.9e-41; Matches 88; Conservative 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fougereau M.;
Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
EMBL, $x03376; CAA27084.1; -; mRNA.

NON TER 1 1 1.

NON TER 98 98
SEQUENCE 98 AA; 11132 MW; 5087889A4CF7298B CRC64;
                                                                                                    119 119 119 AA; 13844 MW; 6B1BC8C7DC77E147 CRC64;
EMBL, X03377; CAA27089.1; -; mRNA.

NON TER 1

NON_TER 119 119

SEQUENCE 119 AA; 13844 MW; 6B1
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                                                                                                                                                                                                                                                      Best Local Similarity
Matches 89; Conserva
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Q53VR2 MOUSE
DD G53VR2 MOUSE
DT 13-SEP-20
DT 13-SEP-20
DT 13-SEP-20
DE VH redion
OC Musmmalia
OC Muridae;
OC Muridae
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61 KPSLKDRISITRDISKNOFFLKLNSVTNEDTATYYCAR 98 61 NPSLKNRISITRDISKNOFFLKLNSVITEDIATYYCAR 98 ò

Search completed: January 10, 2006, 20:53:26 Job time : 79.8731 secs

1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITGGYLMNWIRQFPGNKLEWMGYISYDGTNNY

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Query Match
Best Local Similarity 100.
Matches 112; Conservative
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Sequence 49,
Sequence 61,
Sequence 15,
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Sequence 66,
Sequence 68,
                                                                                                                                                                  January 10, 2006, 20:55:23; Search time 5.71144 Seconds
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Sequence 67,
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1: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

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5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
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(c) 1993 - 2006 Compugen Ltd
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US-11-012-353-67

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US-10-059-310-26

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US-11-012-353-56

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US-11-012-353-57

US-11-012-353-57

US-11-065-943-49

US-11-0693-344-69

US-11-089-266-15

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Maximum Match 100%
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Gaps

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Length 112; Indels

100.0%; Score 595; DB 7; 100.0%; Pred. No. 2.8e-40; tive 0; Mismatches 0;

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US-11-012-353-63
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                                                                                                                                                                                      GENGTH: 112
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TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-198
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT APPLICATION NUMBER: US/35,916
PRIOR PILING DATE: 2003-12-16
PRIOR PILING DATE: 2003-07-11
PRIOR PLILING DATE: 2002-01-20
PRIOR PLILING DATE: 2002-01-20
PRIOR PLILING DATE: 2002-01-18
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APPLICANT: LEGER, OLIVIER
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NECEPTORS ANTIBODIES AND USES THEREOF
TILE REFERENCE: 017753-198
FILE REFERENCE: 017753-196
CURRENT PAPLICATION NUMBER: US/11/012,353
CURRENT FILING DATE: 2004-12-16
PRIOR FILING DATE: 2003-12-16
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-07-11
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Sequence 67, Application US/11012353
Publication No. US20050249730A1
GENERAL INPOMATION:
APPLICANT: GORTSCH, LILIANE
APPLICANT: DUFLOS, ALAIN
APPLICANT: HAGUW, JEAN-FRANCOIS
APPLICANT: LEGER, OLIVIER
APPLICANT: LEGER, OLIVIER
APPLICANT: BECK, ALAIN
APPLICANT: BECK, ALAIN
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Publication No. US20050249730A1
GENERAL INFORMATION:
APPLICANT: GORYSIA, LILIANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: HARUW, JEAN-FRANCOIS
APPLICANT: LEGER, OLIVIER
APPLICANT: BECK, ALAIN
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US-11-012-353-61
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TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
FILE REFERENCE: 01773-198
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT FILING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: RR 0308538
PRIOR APPLICATION NUMBER: FR 0308538
PRIOR APPLICATION NUMBER: FR 0308538
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-07-07
PRIOR FILING DATE: 2003-07-07
PRIOR FILING DATE: 2003-07-07
PRIOR FILING DATE: 2002-01-20
PRIOR FILING DATE: 2002-01-18
PRIOR PRIOR PRIOR DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
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                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 99.8%; Score 594; DB 7; Length 112; Best Local Similarity 99.1%; Pred. No. 3.4e-40; Matches 111; Conservative 1; Mismatches 0; Indels
PRIOR FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: FR 0200653
PRIOR PILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 0200654
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SEQ ID NO 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 63, Application US/11012353;
Publication No. US20050249730A1
GENERAL INFORMATION:
APPLICANT: GORTSCH, LILIANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: LEGER, OLIVIER
APPLICANT: BEGEK, ALAIN
                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
US-11-012-353-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSLLPWTFGQGTKVEIK 112
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 35
                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 102; Conservative
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US-10-959-310-35
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Pred. No. 1.7e-36;
6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 112;
                                                                    Sequence 26, Application US/10959310
Fublication No. US20050287138A1
GENERAL INFORMATION:
APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
TITLE OF INVENTYON: CR4 specific antibody composition
FILE REFERENCE: 249-363
CURRENT FILING DATE: 2004-10-07
PRIOR FILING DATE: 2004-10-07
PRIOR FILING DATE: 2003-15062
PRIOR PLICATION NUMBER: US 60/572,784
PRIOR FILING DATE: 2004-05-21
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 26
LENGTH: 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
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Sequence 33, Application US/10959310

Publication No. US20050287138A1

Publication No. US20050287138A1

GENERAL INFORMATION:

TITLE OP INVENTION: CCR4-specific antibody composition

TITLE OP INVENTION: CCR4-specific antibody composition

FILE REPERENCE: 249-363

CURRENT APPLICATION NUMBER: US/10/959,310

CURRENT PILING DATE: 2004-10-07

PRIOR FILING DATE: 2003-10-08

PRIOR FILING DATE: 2003-10-08

PRIOR FILING DATE: 2004-05-21

NUMBER OF SEQ ID NOS: 46

SSQ ID NO 33

LENGTH: 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
91.9%; Score 547; DB 6;
Best Local Similarity 92.0%; Pred. No. 1.4e-36;
Matches 103; Conservative 5; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Synthetic peptide US-10-959-310-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Synthetic peptide US-10-959-310-33
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Best Local Similarity 91.1%;
Matches 102; Conservative
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1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
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Publication No. US20050287138A1

GENERAL INFORMATION:

TITLE OF INVENTION: CCR4-specific antibody composition

TITLE OF INVENTION: CCR4-specific antibody composition

CURRENT APPLICATION NUMBER: US/10/959,310

CURRENT PILING DATE: 2004-10-07

PRIOR APPLICATION NUMBER: US 60/572,784

PRIOR PILING DATE: 2003-10-08

PRIOR PILING DATE: 2004-05-21
                                                                                 APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
TITLE OF INVENTION: CCR4-specific antibody composition
FILE REFERENCE: 249-326
CURRENT APPLICATION NUMBER: US/10/959,310
CURRENT PILING DATE: 2004-10-07
PRIOR APPLICATION NUMBER: UP 2003-350162
PRIOR PILING DATE: 2003-10-08
PRIOR PILING DATE: 2003-06-08
PRIOR FILING DATE: 2004-05-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
OTHER INFORMATION: Synthetic peptide
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Sequence 34, Application US/10959310
Publication No. US20050287138A1
GENERAL INFORMATION:
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TYPE: PRT
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Publication No. US20050249730A1

GENERAL INFORMATION:

APPLICANT: GOETSCH, LILIANE

APPLICANT: GOETSCH, LILIANE

APPLICANT: DUFLOS, ALAIN

APPLICANT: BECK, ALAIN

APPLICANT: BECK, ALAIN

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

TITLE OF INVENTION NUMBER: US/11/012,353

CURRENT PILING DATE: 2004-12-16

PRIOR APPLICATION NUMBER: FR 0308538

PRIOR FILING DATE: 2003-07-11
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APPLICANT CONVINIA, NATHALIE
APPLICANT CONVINIA, NATHALIE
APPLICANT HAEUW, JEAN-FRANCOIS
APPLICANT HAEUW, JEAN-FRANCOIS
APPLICANT HAEUW, JEAN-FRANCOIS
APPLICANT HAEUW, JEAN-FRANCOIS
APPLICANT HOUSEN OLIVIER
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION NUMBER: 10/135, 916
PRIOR PELING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: FR 0308538
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-07-11
PRIOR PILING DATE: 2002-01-08
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
SEROIR PILING DATE: 2002-01-18
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                                                                                                                                                                                                           Sequence 54, Application US/11012353
Publication No. US20050249730A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Mus musculus US-11-012-353-54
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US-11-U1Z-353-56
Sequence 56, Application US/11012353
Publication No. US2000249730A1
GENERAL INFORMATION:
APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: LEGEN, LILIANE
APPLICANT: LEGEN, LOIVER
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
TITLE OF INVENTION: RECEPTORS ANTIBODIES
CURRENT APPLICATION NUMBER: 10/715-16
PRIOR PILING DATE: 2003-12-16
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2002-01-08
PRIOR FILING DATE: 2002-01-18
PRIOR PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
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90.3%; Score 537; DB 7;
Best Local Similarity 89.3%; Pred. No. 9.2e-36;
Matches 100; Conservative 7; Mismatches 5;
PRIOR APPLICATION NUMBER: PCT/FR03/00178
PRIOR FILING DATE: 2003-01-20
PRIOR APPLICATION NUMBER: FR 0205753
PRIOR APPLICATION NUMBER: FR 0200653
PRIOR FILING DATE: 2002-05-07
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2022-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARE: PATENTIN VOICE: 3.3
SEQ ID NO 49
LENGTH: 122
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ORGANISM: Mus musculus
US-11-012-353-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Mus musculus
US-11-012-353-49
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Best Local Similarity
Matches 98; Conserv
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us-10-735-916a-65.rapbn

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TYPE: PRT ORGANISM: Mus musculus
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| Seneral Information No. US20050287148A1
| GENERAL INFORMATION:
| APPLICANT: Chatterjee, Malaya | APPLICANT: Chatterjee, Malaya | APPLICANT: Chatterjee, Sunil K. | APPLICANT: PRATHENTON: FREATHENT OF MELANOWA AND SMALL CELL CARCINOWA | NUMBER OF SEQUENCES: 66 | CORRESPONDENCE ADDRESS: ADDRESSEE: MCRISON & FOERSTER | STREET: 755 PAGE MILL ROAD | CITY: PALO ALTO | CITY: PALO ALTO | CITY: PALO ALTO | CONTANTOR | CONTANTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                    61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/089,266
FILLING DATE: 23-Mar-2005
                                                                                                                                                                                                                                                            Sequence 23, Application US/11125837
Publication No. US20050266003A1
GENERAL INPORMATION:
APPLICANT: Lin, Rong-Hwa
APPLICANT: Chang, Chung Nan
APPLICANT: Chang, Chung Nan
APPLICANT: Chang, Chunchen
TITLE OF INVENTION: ANTIBODIES
FILE REFERENCE: 13062-011001
CURRENT APPLICATION NUMBER: US/11/125,837
CURRENT APPLICATION NUMBER: US/05-05-10
CURRENT APPLICATION NUMBER: US 60/569,892
PRIOR APPLICATION NUMBER: US 60/569,892
PRIOR FILING DATE: 2004-05-10
NUMBER OF SEQ ID NOS: 100
SEQ ID NO 23
LENGTH: 131
TYPE: FRALESE
CREATION BREATH: 131
CREATH: 131
CREATH: 131
CREATH: 131
CREATH: 131
CREATH: 131
CREATH: 131
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APPLICATION NUMBER: US/10/153,401
FILING DATE: 27-Aug-2002
APPLICATION NUMBER: US 09/293,533
FILING DATE: 1999-04-15
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Sequence 55, Application US/11012353

Publication No. US20050249730A1

GENERAL INFORMATION:
APPLICANT: GOETSCH, LILIANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
APPLICANT: DUFLOS, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-198
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT FILING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: PR 0308538
PRIOR PRILING DATE: 2003-07-11
PRIOR PLILNG DATE: 2002-05-07
PRIOR PLILNG DATE: 2002-05-07
PRIOR PLILNG DATE: 2002-01-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 7; Length 263;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.6%; Score 521; DB 7;
86.6%; Pred. No. 3e-34;
trive 8; Mismatches
APPLICATION NUMBER: US 08/372,676
FILING DATE: 1995-01-17
ATTORNEY AGENT: 1996-01-16
ATTORNEY AGENT INFORMATION:
NAME: Catherine M. Pollazi
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 304142000202
TELEPHONE: (415) 813-5600
TELEPHONE: (415) 813-5600
TELEPHONE: (415) 494-0792
TELEPHONE: (415) 494-0792
TELER: 706141
INPORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARRATERISTICS:
LENGTH: 263 mmino acids
TELENGTH: 263 mmino acids
TELENGTH: 263 mmino acids
TENENG TELESTICE: LENGTH: 263 mmino acids
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SOFTWARE: Patentin Ver. 3.3
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Matches 97; Conservative
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RESULT 15

US-11-012-353-57

i Sequence 57, Application US/11012353

j Publication No. US2056249730A1

j GENERAL INFORMATION:

j APPLICANT: GOSTSH, LILIANE

j APPLICANT: GOSTSH, LILIANE

j APPLICANT: HORNAL NATAALE

j APPLICANT: HEGEN, JEANN

j TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

j TITLE OF INVENTION: NUMBER: 10/1101,353

CURRENT PAPLICATION NUMBER: 10/735,916

pRIOR PILING DATE: 2003-12-16

pRIOR PILING DATE: 2003-12-16

pRIOR PILING DATE: 2003-07-11

pRIOR PILING DATE: 2003-07-11

pRIOR PILING DATE: 2002-05-07

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                                               DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-353-57
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Query Match 87.2%; Score 519; DB 7; Length 112;
Best Local Similarity 85.7%; Pred. No. 2.1e-34;
Matches 96; Conservative 11; Mismatches 5; Indels 0; Gaps 0;
Qy 1 DIVMTQSPLSLEVTPGEPASISCRSSQSIVHSNGNTYLOWYLQKPGQSPQLLIYKVSNRL 60
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Search completed: January 10, 2006, 21:36:23 Job time : 5.71144 secs

Sequence Sequence Sequence Sequence

Sequence Seq

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DIVMIQSPLSLPVIPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
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GENERAL INFORMATION:
APPLICANT: GORYGIA, Inliane
APPLICANT: CORVAIA, Nathalie
APPLICANT: LEGER, Olivier
APPLICANT: LEGER, Olivier
APPLICANT: LEGER, Olivier
APPLICANT: BECK, Alain
APPLICANT: HAEUW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REFERENCE: 0173-143
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REFERENCE: 0173-143
CURRENT APPLICATION NUMBER: US/10/735, 916A
CURRENT APPLICATION NUMBER: PR 03/08 538
PRIOR PELING DATE: 2003-07-11
PRIOR PELING DATE: 2003-01-20
PRIOR PELING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 02/00 654
PRIOR APPLICATION NUMBER: FR 02/00 654
PRIOR PELING DATE: 2002-01-18
PRIOR PELING DATE: 2002-01-18
PRIOR PELING DATE: 2002-05-07
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PATENTIN VET: 2.1
TENGRAL 113
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100.0%; Pred. No. 1.5e-46;
tive 0; Mismatches 0;
US-10-505-980-19
US-10-500-207A-45
US-10-500-207A-45
US-10-231-452-13
US-10-505-980-20
US-09-753-436-66
US-10-163-942-66
US-10-214-452-14
US-10-434-469-40
US-10-505-980-21
US-10-505-980-21
US-10-482-105-38
US-10-505-980-21
US-10-434-469-21
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; Sequence 65, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 112; Conservative
        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-735-916A-65
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182, App
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1 DIVWTQSPLSLPVTPGEPAS.......CFQGSHVPWTFGQGTKVBIK 112
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(cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US03_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
                                                   version 5.1.6
- 2006 Compugen Ltd.
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US-10-433-698-112

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US-10-258-728-28

US-10-258-728-27

US-10-482-105-39

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US-10-500-207A-44

US-10-500-207A-44

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US-10-482-105-39

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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
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Minimum DB Maximum DB

Database

Perfect score:

Sequence:

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Gaps

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Sequence 67, Application US/10735916A Publication No. US20050084906A1

RESULT 2 US-10-735-916A-67

181,

Sequence Sequence

Sequence Sequence Sequence

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Length 112; Indels

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Query Match
Best Local Similarity 99.1
Matches 111; Conservative
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US-10-735-916A-63
US-10-735-916A-61
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SEQ ID NO 63
LENGTH: 131
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US-10-135-9164-0.

Sequence 61, Application US/10735916A

PUBLICARINO. US20050084906A1

GENERAL INFORMATION:

APPLICANT: GOETSCH, Liliane

APPLICANT: CORVALA, Nathalie

APPLICANT: DUFLOS, Alain

APPLICANT: BECK, Alain

APPLICANT: HAEUW, Jean-Francois

TITLE REFERENCE: 017753-183

CURRENT APPLICATION NUMBER: US/10/735,916A

CURRENT APPLICATION NUMBER: US/10/735,916A

FILE REFERENCE: 2003-07-11

FRIOR APPLICATION NUMBER: PR 03/08 538

PRIOR FILING DATE: 2003-07-11

FRIOR PELING DATE: 2003-07-11

FRIOR PELING DATE: 2002-01-18

FRIOR APPLICATION NUMBER: FR 02/00 653

FRIOR APPLICATION NUMBER: FR 02/00 654

FRIOR APPLICATION NUMBER: FR 02/00 654

FRIOR PELING DATE: 2002-01-18

FRIOR PELING DATE: 2002-01-18
                                                 APPLICANT: GOETSCH, LALLHane
APPLICANT: GOETSCH, LALLHane
APPLICANT: CORVAIA, Nathalie
APPLICANT: LEGER, Olivier
APPLICANT: BECK, Alain
APPLICANT: BECK, Alain
APPLICANT: BECK, Alain
APPLICANT: HAEUW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REFERENCE: 0.17753-183
CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT APPLICATION NUMBER: RR 03/08 538
PRIOR PELING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: RR 02/06 653
PRIOR PELING DATE: 2003-01-20
PRIOR PELING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 02/06 653
PRIOR APPLICATION NUMBER: FR 02/06 654
PRIOR APPLICATION NUMBER: FR 02/06 654
PRIOR APPLICATION NUMBER: FR 02/05 753
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100.0%; Score 595; DB 5;
Best Local Similarity 100.0%; Pred. No. 1.8e-46;
Matches 112; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             t TYPE: PRT
CORGANISM: Homo sapiens
US-10-735-916A-67
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ORGANISM: Homo sapiens
GENERAL INFORMATION:
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                                                                                                                                                                                                                                      1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
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Publication No. US20050084906A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GOETSCH, Liliane
APPLICANT: GOETSCH, Liliane
APPLICANT: DEGER, Olivier
APPLICANT: DEGER, Olivier
APPLICANT: DEGER, Olivier
APPLICANT: DEGER, Alain
APPLICANT: HAEUW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-183
CURRENT APPLICATION NUMBER: US/10/735, 916A
CURRENT FILING DATE: 2003-12-16
FRIOR APPLICATION NUMBER: FR 03/00 178
FRIOR APPLICATION NUMBER: FR 03/00 653
FRIOR FILING DATE: 2002-01-18
FRIOR FILING DATE: 2002-01-18
FRIOR FILING DATE: 2002-01-18
FRIOR PELICATION NUMBER: FR 02/00 654
FRIOR FILING DATE: 2002-01-18
FRIOR APPLICATION NUMBER: FR 02/05 553
FRIOR APPLICATION
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Pred. No. 2.2e-46;
1; Mismatches 0; Indels
Length 112;
                                                                                            0; Indels
Score 594; DB 5;
Pred. No. 1.9e-46;
1; Mismatches 0
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APPLICANT: Wu, Dayang
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 1087-37
CURRENT APPLICATION NUMBER: US/10/308,817
CURRENT FILING DATE: 2002-12-03
NUMBER OF SEQ ID NOS: 195
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    99.8%;
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Best Local Similarity 99.19
Matches 111; Conservative
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TITLE OF INVENTION: Anti-fiblioblast growth factor-8 monoclonal antibod
TITLE OF INVENTION: Anti-fiblioblast growth factor-8 monoclonal antibod
TITLE REFERENCE: 249-310
CURRENT APPLICATION NUMBER: US/10/434,469
CURRENT FILING DATE: 2003-05-09
PRIOR PELICATION NUMBER: US 08-081754
PRIOR FILING DATE: 1997-04-03
PRIOR FILING DATE: 1997-04-03
PRIOR PILING DATE: 1997-04-03
PRIOR PILING DATE: 1999-06-07
PRIOR PILING DATE: 1999-06-07
PRIOR PILING DATE: 1099-06-07
PRIOR PILING DATE: US 09/326,590
PRIOR PLING DATE: US 09/876,040
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                                                                                                                                                Query Match 94.8%; Score 564; DB 4; Length 112; Best Local Similarity 94.6%; Pred. No. 1e-43; Matches 106; Conservative 3; Mismatches 3; Indels
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Pred. No. 1e-43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 182, Application US/10453698
Publication No. US20040038308A1
GENERAL INFORMATION:
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 82 CIP (1087-37 CIP)
CURRENT APPLICATION NUMBER: US/10/453,698
CURRENT FILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 196
SOFTWARE: PatentIn version 3.2
IENGTH: 112
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Publication No. US20040091480A1
GENERAL INFORMATION:
APPLICANT: Nobuo HANAI
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SOFTWARE: Patentin version 3.1
SEQ ID NO 182
LENGTH: 112
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Matches 106; Conservative
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Akiko FURUYA
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Kenya SHITARA
Naoki SHIMADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: human
US-10-453-698-182
                                                                                   ; ORGANISM: human
US-10-308-817-182
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US-10-434-469-19
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                                                                 TYPE: PRT
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APPLICANT: KYOWA HAKKO KOGYO CO., LTD
TITLE OF INVENTION: Humanized anti-FGF-8 antibody and the antibody fragment thereof
FILE REPERENCE: 11399WOI
CURRENT APPLICATION NUMBER: US/10/482,105
CURRENT FILING DATE: 2003-12-24
PRIOR FILING DATE: 2001-196176
PRIOR FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 17
LENGTH: 112
                                                                                                                                                                                                           , OTHER INFORMATION: Description of Artificial Sequence: VL synthetic peptide US-10-434-469-19
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Pred. No. 1e-43;
4; Mismatches 2; Indels
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Pred. No. 1e-43;
4; Mismatches 2; Indels
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Publication No. US20050175608A1
GENERAL INPORMATION:
APPLICANT: KYOWA HAKKO KOGYO CO., LTD
TITLE OF INVENTION: AGENT FOR TREATING ARTHRITIS
FILE REFERENCE: 1442
CURRENT APPLICATION NUMBER: US/10/500,207A
CURRENT APPLICATION NUMBER: US/0500.207A
CURRENT APPLICATION NUMBER: J204-06-28
FRIOR APPLICATION NUMBER: J201-400677
PRIOR FILING DATE: 2001-12-28
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17, Application US/10482105
Publication No. US20040253234A1
GENERAL INFORMATION:
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Best Local Similarity 94.6%;
Matches 106; Conservative
                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
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PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 43
SOFWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 112
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Best Local Similarity 94.6'
Matches 106; Conservative
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US-10-500-207A-19
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US-10-500-207A-47
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US-10-258-728-27
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  LENGTH: 112
                                                                                                                                                                  Query Match
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APPLICANT: Bilis, John Robert Maxwell
APPLICANT: Blis, John Robert Maxwell
APPLICANT: Durrant, Linda Gillian
ITILE OF INVENTION: Humanised Antibodies to the Epidermal Growth Factor Receptor
FILE RPERENCE: 26438-1010501
CURRENT PAPLICATION NUMBER: US/10/258,728
CURRENT PILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: GB 0011981.8
PRIOR PILING DATE: 2000-05-19
PRIOR FILING DATE: 2000-06-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.1
LENGTH: 112
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                                                                                                                                                                                   Score 564; DB 5; Length 112;
Pred. No. 1e-43;
4; Mismatches 2; Indels
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APPLICANT: KYOWA HAKKO KOGYO CO., LTD
TITLE OF INVENTION: AGENT FOR TREATING ARTHRITIS
FILE REPERENCE: 1442
CURRENT FILING DAFE: 2004-06-28
FRICH APPLICATION NUMBER: US/10/500,207A
CURRENT FILING DAFE: 2001-12-28
NUMBER OF SEQ ID NOS: 51
SOFTWARE PALENT Version 3.1
SEQ ID NO 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 47, Application US/10500207A Publication No. US20050175608A1
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; Publication No. US20040091485A1
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Best Local Similarity 94.6%;
Matches 106; Conservative
                                           TYPE: PRT
ORGANISM: Artificial Sequence
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US-10-258-728-28
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                     LENGTH: 112
SEQ ID NO 19
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APPLICANT: Ellis, John Robert Maxwell
APPLICANT: Durant, Linda Gillian
TITLE OF INVENTION: Humanised Antibodies to the Epidermal Growth Factor Receptor
FILE REPREBURE: 28438-101US01
CURRENT APPLICATION NUMBER: US/10/258,728
CURRENT FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: GB 0011981.8
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                                                           OTHER INFORMATION: LV.2-2, a designed amino acid sequence of VL of OTHER INFORMATION: an anti-FGF-8 CDR-grafted neutralizing antibody
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APPLICANT: Saldanha, Jose
JITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE BETA
TITLE OP INVENTION: AMYLOID PEPTIDE
FILE REFERENCE: ELN-004
CURRENT APPLICATION NUMBER: US/10/388,214A
CURRENT FILING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: US 60/363,751
PRIOR FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FASTESQ for Windows Version 4.0
SEQ ID NO 6
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                                                                                                                                                                                  Length 112;
                                                                                                                                                                               Score 559; DB 5;
Pred. No. 2.9e-43;
6; Mismatches 2;
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; Publication No. US20040091485A1
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                        Best Local Similarity 92.9
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; LOCATION: (1)...(20)
US-10-388-214A-6
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Sequence 26, Application US/10258728

Sequence 26, Application US/10258728

Sequence 26, Application No. US20040091485A1

SEMENAL INFORMATION:

APPLICANT: BULYANTION:

APPLICANT: DUTRANT, Linda Gillian

TILE REFERENCE: 28438-101US01

TILE REFERENCE: 28438-101US01

TILE REFERENCE: 28438-101US01

FILE REFERENCE: 28438-101US01

FRIOR APPLICATION NUMBER: GB 0011981.8

FRIOR FILING DATE: 2000-05-19

FRIOR FILING DATE: 2000-08-24

NUMBER OF SEQ ID NOS: 28

SOFTWARE PARENTIN VERSION 3.1

SEQ ID NO SEC ID NOS: 28

LENGTH: 112
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                                                                                                                                                                                                                                                                                              1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                                                                                                                                                                                                                                          0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                          Score 557; DB 4; Length 112;
Pred. No. 4.4e-43;
4; Mismatches 5; Indels
                                                                                                                                                                                                                 Length 112;
                                                                                                                                                                                                                                                        5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: KYOWA HAKKO KOGYO CO., LTD
TITLE OF INVENTION: AGENT FOR TREATING ARTHRITIS
FILE REFERENCE: 1442
CURRENT APPLICATION NUMBER: US/10/500,207A
CURRENT FILING DATE: 2004-06-28
PRIOR APPLICATION NUMBER: JP2001-400677
PRIOR FILING DATE: 2001-12-28
NUMBER OF SEQ ID NOS: 51
                                                                                                                                                                                                                 Score 558; DB 4;
Pred. No. 3.5e-43;
4; Mismatches 5
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: GB 0020794.4
PRIOR FILING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Version 3.1
SEQ ID NO 27
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, Sequence 46, Application US/10500207A

, Publication No. US20050175608A1

, GENERAL INFORMATION:
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Best Local Similarity 92.0%;
Matches 103; Conservative
                                                                                                                                                                                                             Query Match
Best Local Similarity 92.04
Matches 103; Conservative
                                                                                                                                  ; TYPE: PRT
; ORGANISM: Mus musculus
US-10-258-728-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Mus musculus US-10-258-728-26
                                                                                                                        LENGTH: 112
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STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
RESULT 1
 January 10, 2006, 20:34:27; Search time 21.8706 Seconds (without alignments) 423.384 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                   1 DIVMTQSPLSLPVTPGEPAS......CFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 50,
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(cgn2_6/ptodata/1/iaa/5_COMB.pep:*

// cgn2_6/ptodata/1/iaa/6_COMB.pep:*

// cgn2_6/ptodata/1/iaa/H_COMB.pep:*

// cgn2_6/ptodata/1/iaa/PGTUS_COMB.pep:*

// cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

// cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

// cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
           GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-331-398A-50
US-08-331-397B-50
US-08-227-693-50
US-08-015-190A-14
US-08-482-882-66
US-08-483-389-66
US-08-487-113D-66
US-08-487-113D-66
US-08-487-113D-66
US-08-487-113D-66
US-08-473-503-66
US-08-473-503-66
US-08-773-503-66
US-08-773-680-65
US-08-775-880-95
US-08-134-346A-50
US-08-176-288A-95
US-08-176-349A-88
US-08-176-349A-88
US-08-176-349A-88
US-08-176-349A-88
US-08-176-349A-88
US-08-176-349A-88
US-08-176-349A-86
US-08-176-349A-86
US-08-176-349A-86
US-08-176-349A-86
US-08-176-349A-86
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US-08-077-252B-3
US-08-331-397B-48
US-08-759-804A-48
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                                                                                                                                                                                      572060 segs, 82675679 residues
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Maximum Match 100%
Listing first 45 summaries
                                                    - protein search, using sw model
                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                              US-10-735-916A-65
595
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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                                                    OM protein
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                                                                       Run on:
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        28
        519
        87.2
        112
        2
        US-09-002-753A-3
        Sequence 48, Appliance 49, Appliance 48, Appliance 49, Appliance 4
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#### TT GIVER

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NEGULAT 198A-50

1 Sequence 50, Application US/08331398A

Patent No. 560803

1 GENERAL INFORMATION:

APPLICANT: Patent, ITA

APPLICANT: Patent, ITA

APPLICANT: Patent, ITA

APPLICANT: Patent, Ulrich

APPLICANT: San Francisco

STREET: California

CONFUTE: San Francisco

STREET: California

COMPUTE: USA

STREET: Patentin Release #1.0, Version #1.30

SOFTWARE: Patentin Release #1.0, Version #1.30

CURTY: San Francisco

SOFTWARE: Patentin Release #1.0, Version #1.30

CURTY: San Francisco

SOFTWARE: Patentin Release #1.0, Version #1.30

CURTY: San Francisco

SOFTWARE: 12406-1994

FILING DATE: 12-0C-1994

FILING DATE: 13-0C-1994

FILING DATE: 13-0C-1994

TELECOMONINICANTON NUMBER: US 07/596,289

FILING DATE: 13-0C-1994

TELECOMONINICANTON NUMBER: US 07/596,289

FILING DATE: 13-0C-1994

TELECOMONINICANTON NUMBER: US 07/596,289

TELECOMONINICANTON NUMBER: US 07/596,289
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Query Match
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Patent No. 5981726
GENERAL INFORMATION:
APPLICANT: Pastenn, Ira
APPLICANT: Benhar, Itai
TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
TITLE OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                     1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
                                                                                                                                                                                                                                                                                                      0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                         61 SCVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCPQGSHVPFTFGQGTKVEIK 112
                                                                                                                                                               Length 112;
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US-08-331-3978-50
                                                       /note= "Humanized B3 Variable Light
chain (V-L) (HumB3V-L)"
                                                                                                                                                          Query Match
93.9%; Score 559; DB 1; Length 11:
Best Local Similarity 93.8%; Pred. No. 2.6e-47;
Matches 105; Conservative 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: ISM PC COMPATIBLE
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Plaza
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/331,397B
FILING DATE: 28-OCT-1994
CLASSIFICATION NUMBER: US/08/331,397B
FILING DATE: 28-OCT-1994
GLASSIFICATION: 435
FRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: HULTEY, TOW
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126120US
TELEPAX: (415) 543-560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
h NAME/KEY: Protein IOCATION: 1..112
OTHER INFORMATION:
OTHER INFORMATION:
US-08-331-398A-50
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1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
                                                                                              Gaps
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Score 559; DB 1; Length 112;
Pred. No. 2.6e-47;
4; Mismatches 3; Indels
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15-08-759-804A-50

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chain (V-L) (HumB3V-L)"
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,804A
FILING DATE: 03-DEC-1996
CLASSIFICATION 356
PRIOR APPLICATION NUMBER: US/08/331,398
FILING DATE: 28-OCT-1994
PRIOR APPLICATION NUMBER: US 08/331,398
FILING DATE: 28-OCT-1994
PRIOR APPLICATION NUMBER: US 07/767,331
PRIOR APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION NUMBER: US 07/56,289
FILING DATE: 12-OCT-1990
ATTOMENYAGEN: 110-OCT-1990
ATTOMENYAGEN: 110-OCT-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATION SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Weber, Ellen L.
REGISTRATION INUBER: 32,762
REFRENCE/DOCKET NUMBER: 0152
TELECOMMUNICATION INFORMATION:
TELEFONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 50:
        93.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 112 amino acids
amino acid
                                                 Best Local Similarity 93.8
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS LENGTH: 112 amino acic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COCATION: 1..112
COTHER INFORMATION:
COTHER INFORMATION:
US-08-759-804A-50
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/note= "Residue that has been replaced with mouse amino acid in the humanized
                                                                                                                                                                                                                       61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCPQGSHVPFTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Complementarity-determining
region"
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region"
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                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
US-08-053-171-15
Sequence 15, Application US/08053171
Sequence 15, Application US/08053171
Sequence 15, Application US/08053171
Sequence 15, Application US/08053171
Sequence 15, Application of General Application of True Co. Loibner
TITLE OF INVENTION: Antibody Derivatives
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS: ADDRESSE: Townsend and Townsend Khourie and Crew STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: P4301

COMPUTER: FLORDY disk

MEDIUM TYPE: Floryy disk

COMPUTER: TEN PC compatible

COMPUTER: TEN PC compatible

CORFRAING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/053,171

FILING DATE: 22-APR-1993

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Smith, Willaim M

REFERENCE/DOCKET NUMBER: 11823-54-1

TELEPHONE: (415) 326-2400

TELEPHONE: (415) 326-2422

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 112 amino acids

TYPE: amino acid

TYPE: AND COMPUTED 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Peptide
LOCATION: 1..112
OTHER INFORMATION: /note= "Sequence of the Light
Patent No. 5552903
OTHER INFORMATION: of Humanized BR55-2 Antibody"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              region"
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LOCATION: 94.102
OTHER, INFORMATION: region'
FEATURE:
NAME/KEY: Modified-site
LOCATION: 54
OTHER INFORMATION: rogion'
OTHER INFORMATION: region'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEATURE:
NAME/KEY: Region
LOCATION: 24.39
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
NAME/KEY: Region
LOCATION: 55.61
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94301
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                                                                                                             1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
                                                                                                                                                                                    1 DVLMTQSPLSLPVTPGEPASISCRSSQIIVHSNGNTYLEWYLQKPGQSPQLLIYKVSNRF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-UN-16/10/2019

Sequence 50, Application US/09227693

Factont No. 6287562

GENERAL INFORMATION:

APPLICANT: BENHAR, Itai

APPLICANT: WING, SUN-Hee

APPLICANT: WING, SUN-Hee

APPLICANT: WING, SUN-Hee

APPLICANT: WING, SUN-HEE

APPLICANT: STORMENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSES: Townsend and Townsend Khourie and Crew

STREET: Steuart Street Tower, One Market Plaza

CITY: San Francisco

STARET: California

CONDIEX: US

ZIP: 94105-1493

COMPUTER: READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/227, 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                    0; Gaps
                                                                                                                                                                                                                                                                                                      61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                             61 SGVPDRPSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPFTFGQGTKVEIK 112
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        Best Local Similarity 93.8%; Pred. No. 2.6e-47;
Matches 105; Conservative 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: 1..112
; OTHER INFORMATION: /note= "Humanized B3 VL region"
US-09-227-693-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION DATA:
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/331,396
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-0CT-1990
ATTONEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 15280-126-1-3
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ 1D NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acide
TYPE: Amino Amino
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Protein
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                                                                                                                                                                                                                                                                                          Gaps
                                                                                                /note= "Residue in the framework that is replaced with mouse amino acid in the humanized antibody."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPFTFGQGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVBIK 112
                                                                                                                                                                                                                                 Query Match 93.6%; Score 557; DB 1; Length 112; Best Local Similarity 94.6%; Pred. No. 4.1e-47; Matches 106; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "mature light chain variable
region of humanized ABL 364 antibody"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/08815190A
Patent No. 6046310
GENERAL INFORMATION:
APPLICANT: Oueen, Cary L.
APPLICANT: Schneider, William P.
APPLICANT: Vaequez, Maximilian P.
TITLE OF INVENTION: Uses Ligand Fusion Proteins and Their
TITLE OF INVENTION: Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOGTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,190A
FILING DATE: 11-MAR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/614,584
FILING DATE: 13-MAR-1996
ATTORNEY/AGENT INPORMATION:
NAME: Apple: Randolph T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS: 17
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REPERENCE/DOCKET NUMBER: 011823-006710US
TELECOMMUNICATION INPORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS:
OTHER INFORMATION: antibody."
                   FEATURE:
NAME/KEY: Modified-site
LOCATION: 108
OTHER INFORMATION: that i
OTHER INFORMATION: that i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
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COTHER INFORMATION:

COTHER INFORMATION:

CS-08-815-190A-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-815-190A-14
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                                                                                                               1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
                                                            0; Gaps
                                                                                                                                                                                                                                                     61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPFFFGQGTKLEIK 112
                                                                                                                                                                                                                            61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                   US-08-482-86
; Sequence 66, Application US/08482882
; Patent No. 5773218
; GENERAL INFORMATION:
    APPLICANT: Gallatin, W. Michael
    APPLICANT: Oxecux, Rosemay
    TITLE OF INVENTION: ICAM-Related Materials and Methods
    NUMBER OF SEQUENCES: 116
    CORRESPONDENCE ADDRESS:
    ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun
    STREET: G300 Sears Tower, 233 S. Wacker Drive
    STREET: Illinois
    STREET: Illinois
Query Match 93.6%; Score 557; DB 2; Length 112; Best Local Similarity 94.6%; Pred. No. 4.1e-47; Matches 106; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 544; DB 1; Length 116;
Pred. No. 7.8e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: W-LUS/MS-BUS
OPERATING SYSTEM: W-LUS/MS-BUS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,882
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/286,754
FILING DATE:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION NUMBER: US 08/009,266
FILING DATE: 25-AN-1993
PRIOR APPLICATION NUMBER: US 07/894,061
FILING DATE: 25-JAN-1993
PRIOR APPLICATION NUMBER: US 07/894,061
FILING DATE: STAN-1992
PRIOR APPLICATION NUMBER: US 07/894,061
FILING DATE: STAN-1992
PRIOR APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-ANN-1992
PRIOR APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-ANN-1992
PRIOR APPLICATION NUMBER: US 07/889,734
APPLICATION NUMBER: US 07/827,689
FILING DATE: 1700-NUMBER: 37,302
PREGESTRATION NUMBER: 35,302
PREGESTRATION NUMBER: 35,302
PREGESTRATION NUMBER: 35,302
PREPERPENT NUMBER: 35,302
PREPERPENT NUMBER: 37,318
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TELECOMMUNICATION INFORMATION:
TELEPAX: (312) 474-6300
TELERAX: 25-3856
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.4%;
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MOLECULE TYPE: protein
US-08-482-882-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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5 DIVMTQSPLSLPVTPGEPASISCRSSQSLVHSNGDTYLHWYLQXPGQSPQLLIYKVSNRF 64
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                                                               61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                               65 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTHVPYTFGQGTKVEIK 116
                                                                                                                                                                                          RESULT 9
US-08-487-113D-66

JOS-08-487-113D-66

JESTIN NO. 583790

JESTIN NO. 583790

JESTIN NO. 583790

JESTIN GALLANT: GALLATIN, W. Michael

APPLICANT: Vazeux, Rosemay

TITLE OF INVENTION: ICAM-Related Materials and Methods

NUMBER OF SEQUENCES: 120

CORRESPONDENCES: 120

JOSESSER: Marchall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

COUNTRY: United States of America

CONFITER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: IBM PC compatible

OPRESTATING SYSTEM: PC-CDOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

PITING DAMPS.

PATING DAMPS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 91.4%; Score 544; DB 1; Length 116; Best Local Similarity 92.0%; Pred. No. 7.88-46; Matches 103; Conservative 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,754
FILING DATE: 05-AUG-1994
PRIOR APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-AN-1993
PRIOR APPLICATION NUMBER: US 07/894,061
FILING DATE: 22-AN-1993
PRIOR APPLICATION NUMBER: US 07/894,061
FILING DATE: 26-MX-1992
PRIOR APPLICATION NUMBER: US 07/899,724
FILING DATE: 26-MX-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/897,689
FILING DATE: 27-AN-1992
ATTORNEY AGENT INFORMATION:
NAME: NO. 5837822AAG, Greta E.
REGISTRATION NUMBER: 35,3022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 32744
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 116 amino acids
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-487-113D-66
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                                                               1 DIVMIQSPLSLPVIPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
                                                                                               5 DIVMIQSPLSLPVIPGEPASISCRSSQSLVHSNGDTYLHWYLQKPGQSPQLIYKVSNRF 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
         0; Gaps
                                                                                                                                                                                       61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                       65 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTHVPYTFGQGTKVEIK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                              PETERIE INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, R. Sesmay
TITLE OF INVENTION: ICAM-RELATED PROTEIN
NUMBERS OF SEQUENCES: 118
CORRESPONDERS MATCHALL, O'TOOLe, Gerstein, Murray & Borun
STREET: 213 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STREET: 213 South Wacker Drive/6300 Sears Tower
CITY: United States of America
CONTRY: LILING SYSTEM: PC-DOS/MS-DOS
SOUTHER: IDADIAN PC-CHOS/MS-DOS
SOUTHARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 07-JUN-1995
CIASSIFICATION NUMBER: US 08/102,852
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 28-MA-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 28-MA-1992
RECOMMENTION NUMBER: US 07/894,061
FILING DATE: 28-MA-1992
RECOMMENTION NUMBER: US 07/894,061
FILING DATE: 28-MA-1992
RECOMMENTION NUMBER: US 07/894,061
FILING DATE: 28-MA-1992
REPRENCE OF TELECOMMUNICATION NUMBER: US 07/894,061
FILING DATE: 28-MA-1992
REPRENCE OF TELECOMMUNICATION NUMBER: US 07/894,061
FILING DATE: 28-MA-1992
REPRENCE OF TELECOMMUNICATION NUMBER: US 07/894,061
FILING DATE: 28-MA-1992
REPRENCE OF TELECOMMUNICATION NUMBER: US 07/894,061
FILING DATE: 38-MA-1992
REPRENCE OF TELECOMMUNICATION NUMBER: US 07/894,061
FILING DATE: 38-MA-1992
REPRENCE OF TELECOMMUNICATION NUMBER: US 07/894,061
FILING DATE: 38-MA-1992
REPRENCE OF TELECOMMUNICATION NUMBER: US 07/894,061
FILING DATE: 38-MA-1992
REPRENCE OF TELECOMMUNICATION NUMBER: US 07/894,061
FILING DATE: 38-MA-1992
REPRENCE OF TELECOMMUNICATION NUMBER: US 07/894,061
FILING DATE: 38-MA-1992
REPRENCE OF TELECOMMUNICATION OF 08-MA-1992
REPRENCE OF TELECOMMUNICATION OF 08-MA-1992
REPRENCE OF 08-MA-1992
REPRENCE OF 
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      5; Indels
         4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 66, Application US/08483389
Patent No. 5811517
         Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-389-66
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Gaps

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us-10-735-916a-65.rai

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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                     61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 544; DB 1; Length 116;
Pred. No. 7.8e-46;
4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 S. Wacker Drive CITY: Chicago STATE: 1llinois COUNTRY: USA ZIP: 60606
                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/473,503

FILING DATE: 0'-JUN 1995

CLASSIFICATION NUMBER: US/08/473,503

FILING DATE: 0'-JUN 1995

PILING DATE: 05-AUG-1994

APPLICATION NUMBER: US 08/102,852

PILING DATE: 05-AUG-1993

PRIOR APPLICATION NUMBER: US 08/09,266

PILING DATE: 25-ANN-1993

PRIOR APPLICATION NUMBER: US 08/09,266

PILING DATE: 22-JAN-1993

PRIOR APPLICATION NUMBER: US 07/894,061

PILING DATE: 26-AUX-1992

PRIOR APPLICATION NUMBER: US 07/894,061

PILING DATE: 26-AUX-1992

PRIOR APPLICATION NUMBER: US 07/889,724

FILING DATE: 26-AUX-1992

ATTORNEY/AGENT INFORMATION:

NAME: NO. 5862562and, Greta E.

REGISTRATION NUMBER: 32.73

TELECOMMUNICATION NUMBER: 33.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC_DOS/MS-DOS
                                                                                                                                                      Sequence 66, Application US/08473503 Patent No. 5869262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-6448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acids
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Best Local Similarity 92.0%;
Matches 103; Conservative
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US-08-473-503-66
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1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
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YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
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                                                                                                                                                US-08-483-932-66
; Sequence 66, Application US/08483932
; Patent No. 5880268
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: GALLACH: ICAM-Related Materials and Methods
; TITLE OF INVENTION: ICAM-Related Materials and Methods
; TINDERS OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITT: Chicago
; STATE: Illinois
; COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 91.4%; Score 544; DB 1; Length 116; Best Local Similarity 92.0%; Pred. No. 7.8e-46; Matches 103; Conservative 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,932
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA

APPLICATION NUMBER: 08/286,754

FILING DATE: 05-AUG-1994

APPLICATION NUMBER: US 08/102,852

FILING DATE: 05-AUG-1993

PRIOR APPLICATION NUMBER: US 08/009,266

FILING DATE: 22-JAN-1993

PRIOR APPLICATION NUMBER: US 07/894,061

FILING DATE: 05-JUN-1992

PRIOR APPLICATION NUMBER: US 07/894,061

FILING DATE: 05-JUN-1992

PRIOR APPLICATION NUMBER: US 07/899,724

FILING DATE: 26-MAY-1992

PRIOR APPLICATION NUMBER: US 07/827,689

FILING DATE: 27-JAN-1992

ATTORNEY/AGENT INFORMATION:
NAME: NO. S8802688nd, Greta E.

REGISTRATION NUMBER: 331.78

REGISTRATION NUMBER: 331.78

TERECOMMINICATION INFORMATION:
NAME: NO. S8802688nd, Greta E.

REGISTRATION NUMBER: 331.78

TERECOMMINICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 66:
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65 SGVPDRPSGSGSGTDFTLKISRVEAEDVGVYYCSQSTHVPYTFGQGTKVEIK 116
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FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAX-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 21-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6040176and, Greta E.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 32178
TELECOMMINICATION: TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
PALLICATION NUMBER: 08/286,754
FILING DATE:
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92.0%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                  US-08-714-017-66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 DIVMTQSPLSLPVTPGEPASISCRSSQSLVHSNGDTYLHWYLQKPGQSPQLLIYKVSNRF 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                     COUNTRY: Chicago
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: 11inois
COUNTRY: United States of America
ZIP: 6060-6402
COUNTRY: United States of America
ZIP: 6060-6402
COMPUTER: ELOPPY disk
COMPUTER: ELOPPY disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/720,420A
PILING DATE:
CLASSIFICATION NUMBER: US/08/720,420A
PRIOR APPLICATION NUMBER: US 08/487,113
FILING DATE: 07-JUM-1995
PRIOR APPLICATION NUMBER: US 08/487,113
FILING DATE: 05-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
PRIOR APPLICATION NUMBER: US 08/102,852
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
PRIOR APPLICATION NUMBER: US 08/102,852
PRIOR APPLICATION NUMBER: US 07/894,061
FILING DATE: 22-JAN-1993
PRIOR APPLICATION NUMBER: US 07/894,061
FILING DATE: 26-MAY-1992
PRIOR APPLICATION NUMBER: US 07/894,061
FILING DATE: 26-MAY-1992
PRIOR APPLICATION NUMBER: US 07/897,689
FILING DATE: 26-MAY-1992
PRIOR APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY JASENT INFORMATION:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY JASENT INFORMATION:
ANDRE: 27-JAN-1992
ATTORNEY JASENT INFORMATION:
ANDRE: 27-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.4%; Score 544; DB 1; Length 116; 92.0%; Pred. No. 7.8e-46;
                                                                         WS-08-720-420A-66

Sequence 66, Application US/08720420A

Patent No. 5989843

GENERAL INFORMATION:

APPLICANT: Gallatin, W. Michael

APPLICANT: Vazeux, Rosemay

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 120

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Williams, Joseph A., Jr.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 33282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 66: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 116 amino acids
amino acid
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Matches 103; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
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Pred. No. 7.8e-46;
4; Mismatches 5; Indels
Sequence 66, Application US/08714017
Patent No. 6040176
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                     ZIP: 6666
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTEN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,017
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5 DIVWIQSPLSLPVIPGEPASISCRSSQSLVHSNGDTYLHWYLQKPGQSPQLIYKVSNRF 64
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RESULT 14
US-08-475-680-66

Sequence 66, Application US/08475680

Sequence 100383

Patent No. 6100383

APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay

TITLE OF INVENTION: ICAM-Related Materials and Methods

NUMBER OF SEQUENCES: 116

CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 S. Wacker Drive

CITY: Chicago

STATE: 1111nois

COUNTRY: USA
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Pred. No. 7.8e-46;
4; Mismatches 5; Indels
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COUNTRY:

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COUNTRY:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER:

SYSTEM:

PC-DOS/MS-DOS

SOFTWARE:

PRICATION NUMBER:

MEDIUM TAPLICATION DATA:

APPLICATION NUMBER:

MEDIUM TAPLICATION NUMBER:

PILING DATE:

MAPLICATION NUMBER:

MEDIUM TAPLICATION NUMBER:

MEDIUM TAPLICATION NUMBER:

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Best Local Similarity 92.0%;
Matches 103; Conservative
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1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
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Sequence 95, Application US/08129930B
; Betent No. 5804187
; GENERAL INFORMATION:
    APPLICANT: do Couto Dr., Fernando J.R.
    APPLICANT: Ceriani Dr., Roberto L.
    APPLICANT: Padian Dr., Betuardo A.
    APPLICANT: Padian Dr., Jerry A.
    APPLICANT: Padian Dr., Betuardo A.
    TITLE OF INVENTION: Carcinoma Specificity, and Kit and TITLE OF INVENTION: Therapeutic Methods
    TITLE OF INVENTION: Therapeutic Methods
    NUMBER OF SEQUENCES: 96
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: V. AMZEL & ASSOC.
    STREET: 2055 NO. 5804187th Broadway, Suite 201
    CITY: Walnut Creek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 91.3%; Score 543; DB 1; Length 131; Best Local Similarity 90.2%; Pred. No. 1.1e-45; Matches 101; Conservative 7; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: END PC compatible
COMPUTER: END PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/129,930B
FILING DATE: September 30, 1993
CLASSIFICATION: 424
ATYONREY/AGENT INFORMATION:
NAME: Anneal Ph.D., Viviana
REGISTRATION NUMBER: 30,930
REPRENCE/DOCKET NUMBER: 30,930
REPRENCE/DOCKET NUMBER: GRECC-008A
TELECOMMUNICATION INFORMATION:
TELEFRAK: (510) 521-333
TELEFRAK: (510) 521-333
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TYPE: amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: peptide
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Search completed: January 10, 2006, 20:58:03 Job time : 21.8706 secs

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Homo sapiens (Human).
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                                                     January 10, 2006, 20:26:41 ; Search time 75.5025 Seconds (without alignments) 1046.577 Million cell updates/sec
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                                                                                          US-10-735-916A-65
595
1 DIVMTQSPLSLPVTPGEPAS......CRQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                               Description
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                              2166443 seqs, 705528306 residues
                                                                                                                                                                                                                                                                                                                                                                                                Q652Q7_9MURI
KV2E HÜMAN
WV2F_HÜMAN
WV2F_HÜMAN
WV2D HÜMAN
Q9ULBO_HÜMAN
Q9ULBO_HÜMAN
Q65F210 MÜUSE
WV2G MÜUSE
WV2G MÜUSE
G675D_HÜMAN
G65F20 MÜUSE
G55ZC0 WÜUSE
WV2E HÜMAN
G65XCG MÜUSE
WV2E HÜMAN
G65XCG MÜUSE
WV2E HÜMAN
G65XCG MÜUSE
WV2F MÜUSE
WV3F MÜUSE
                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                     - protein search, using sw model
                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                      UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 2000000000
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Match Length DB
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Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
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                                      OM protein
                                                                                                                                                                                                                                                                        Database :
                                                                                                                                                                Searched:
                                                        Run on:
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P18135 homo sapien Q9u178 homo sapien P01657 homo sapien P01667 mus musculu Q6kb05 mus musculu P01619 homo sapien P01619 homo sapien P01619 homo sapien P01666 mus musculu P01668 mus musculu P01669 mus musculu P01669 mus musculu P01669 mus musculu Q52164 mus musculu		ta; Buteleostomi; dentia; Sciurognathi; ham M., Pastan I.; t causes complete . CRC64; Indels 0; Gaps 0;	(Fragment).
368 61.8 129 1 KV3L HUMAN 361 60.7 109 2 Q9UL78 HUMAN 360.5 60.6 111 1 KV3E HUMAN 360.5 60.6 111 1 KV3E MOUSE 359 60.3 120 1 KV2B MOUSE 357 60.0 120 1 KV2B MOUSE 357 60.0 120 1 KV3A HUMAN 356.5 59.8 129 1 KV3H HUMAN 356.5 59.6 111 1 KV3P MOUSE 354.5 59.6 110 1 KV3P MOUSE 353.5 59.4 111 1 KV3P MOUSE 353.5 59.4 240 2 Q52L64_MOUSE	ALIGNMENTS	## 11   1   1   1   1   1   1   1   1	in V-II region GM607 precursor (Human).
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                                                                                                                                      This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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01-JAN'-1988 (Rel. 06, Last sequence update)
01-JAN'-1988 (Rel. 06, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
1g kappa chain V-II region RPMI 6410 precursor.
Homo sapiens (Human)
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                               Klobeck H.G., Solomon A., Zachau H.G.; "Contribution of human V kappa II germ-line genes to light-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                 kappa chain V-II region GM607
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Pred. No. 3.1e-44;
2; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                               Framework-1.
Complementarity-determining-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Framework-3.
Complementarity-determining-3.
Framework-4.
                                                                                                                                                                                                                                                                                                                               PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin domain; Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12664 MW; 92C57DC719E558B1 CRC64;
                                                                                                                                                                                                          EMBL; Z00009; -; NOT_ANNOTATED_CDS; Genomic_DNA. PIR; A01889; K2HCM.
HSSP; Q99M3; 1191.
SMR; P060309; 5-117.
GO; GO:0005576; C:extracellular region; NAS. GO; GO:0005575; E:antigen binding; NAS. InterPro; IPR00319; P:antigen binding; NAS. InterPro; IPR00319; P:antigen binding; NAS. InterPro; IPR003110; Ig-1ike.
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                                                         NUCLEOTIDE SEQUENCE.
MEDLINE=84191506; PubMed=6325927;
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NUCLEOTIDE SEQUENCE.
MEDLINE=86041852; PubMed=2997711;
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86.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 83.9 Best Local Similarity 86.6 Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                  Nature 309:73-76(1984)
                                                                                                                                                                                                                                                                                                                     SMART; SM00406; IGv; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 117 117 AA;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6410.
Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G., "Human immunoglobulin kappa light chain genes of subgroups II and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig kappa chain V-II region RPMI Framework-1.
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Pred. No. 3.7e-44;
9; Mismatches 9; Indels
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PIR; A01890; KZHURP.

RISP; Q90877; 1191.

SWR; Po6310; Z1-133.

Ensembl; ENSG0000173758; Homo sapiens.

GO; GO:0005576; C:extracellular region; NAS.

GO; GO:0006557; P:immune response; NAS.

InterPro; IPR007110; Ig-like.

InterPro; IPR007110; Ig-like.

InterPro; IPR007110; Ig-like.

InterPro; IPR00835; IG LIKE; 1.

PROSITE; PS50835; IG LIKE; 1.
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Q8NEKO;
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Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan F.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Murxy D.M., Sodergran E.J., Lu X., Gibbs R.A., A Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., A Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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KI Klein R., Jaenichen R., Zachau H.G.;

KI Klein R., Jaenichen R., Zachau H.G.;

L. Eur. J. Immunol. 23:3248-3266(1993).

R. Expressed human immunoglobulin kappa genes and their hypermutation.";

R. Embl. BC030814; AAH30814.1; -; mRNA.

R. FIR; S34091; S34091.

R. FIR; S40342; S40342.

R. FIR; S40357; S40357.

R. RSP; PO1834; 1172.

R. RSP; PO1834; 1172.

R. RSP; QRNEKO; 21-237.

R. RICEPPO; IPRO03106; Ig_MHC.

R. InterPro; IPRO03596; Ig_V.

R. FEm; PF07654; C1-set; 1.

R. SMART; SM00406; IG_WHC.

DR. RMART; SM00406; IG_WHC; UNIXNONN_1.
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"Ongoing V kappa-J kappa recombination after formation of a productive
V kappa-J kappa coding joint."; V kappa-J kappa coding joint."; Eur. J. Immunol. 22:1561-1565 (1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIVMTQSPLSLPVTPGEPASISCRSSQSLTHSDGYNYLDWYLQKPGQSPQLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                               Wagner S.D., Luzzatto L.;
"V kappa gene segments rearranged in chronic lymphocytic leukemia are
distributed over a large portion of the V kappa locus and do not show
somatic mutation.";
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 239 Aa; 26024 MW; F5E20AD3B0552C0A CRC64;
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84.8%; Pred. No. 9.3e-44;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last amnotation update)
1g kappa chain V-II region TEW.
1d kappa chain Wall region TEW.
Elwaryota, Menazoa, Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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Glenner G.G.;
"Structural identity of Bence Jones and amyloid fibril proteins in a patient with plasma cell dyscrasia and amyloidosis.";
J. Ciln. Invest. 52:1276-1281(1973).
-!- MISCELLANBOUS: The major amyloid protein appears to be identical with the Bence Jones protein isolated from the same patient.
-!- MISCELLANBOUS: This protein was isolated from the same patient.
-- PAGSCELLANBOUS: This protein was isolated from the urine of a patient with plasma cell dyscrasia and amyloidosis.
-!- MISCELLANBOUS: The C region of this chain has the INV (1,2)
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                                                                                                                                                                                                                                                                                                                                       PROTEIN SEQUENCE (BENCE-JONES PROTEIN TEW).
MEDLINE=74148480; PubMed=4596149;
Putnam F.W., Whitley B.J. Jr., Paul C., Davidson J.N.;
Manino acid sequence of a kappa Bence Jones protein from a case
primary amyloidosis.";
Biochemistry 12:3763-3780(1973).
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R SMR; PO1617; 1-113.
R GO; GO:0005576; C:extracellular region; NAS.
R GO; GO:0005823; F:antigen binding; NAS.
R GO; GO:0006955; P:antigen briding; NAS.
R GO; GO:0006955; P:antigen briding; NAS.
R InterPro; IPR007110; Ig-1ike.
R InterPro; IPR003596; Ig-V.
R SMART; SMO04106; IGV.
DR RNOSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR Amyloid; Bence-Jones protein; Direct protein sequencing; KW Immunoglobulin domain; Immunoglobulin V region.

I 23 Franchonestiv-determining-1.
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Complementarity-determining-3.
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MEDLINE=73166638; PubMed=4700495;
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SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWPPWTFGQGTKVEIK 113
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   61
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                                                                                                         RESULT 7

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OSF210-MO

DT 10-M

DT 10-M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DVVMTQSPLSLPVTLRQPASISCRSSQSPVYSDGNTYLNWFQQRPGQSPRALIYKVSNRD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=1601042;
Huber C., Klobeck H.G., Zachau H.G.;
"Ongoing V kappa-J kappa recombination after formation of a productive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stuber F., Lee S.K., Bridges S.L. Jr, Koopman W.J., Schroeder H.W. Jr, Gaskin F., Fu S.M.;
"A rheumatoid factor from a normal individual encoded by VH2 and V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wagner S.D., Luzzatto L.; "V kappa gene segments rearranged in chronic lymphocytic leukemia are distributed over a large portion of the V kappa locus and do not show
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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   SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMZALQAPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.4%; Score 484.5; DB 2; Length 114; 83.2%; Pred. No. 1e-42; live 8; Mismatches 10; Indels 1
                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 AA; 12775 MW; 070E31E210D1CB01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in. Immunol. Immunopathol. 87:184-192(1998).
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Eur. J. Immunol. 22:1561-1565(1992).

EmBL; AR038034; AAD56270.1; -; mRNA.

PIR; B49002; B49002.

PIR; S23638; S23638.

PIR; S34094; S34094.

PIR; S34095; S34095.

HSSP; P01652; 11V4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                kappa II gene segments.";
Arthritis Rheum. 35:900-904(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                 QULBO_HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 83.2
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       somatic mutation."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=8436174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                      HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 41, Last annotation update)
10-MAY-2005 (Rel. 47, Last annotation update)
119 kappa chain V-II region 26-10.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Musinae; Mus.
                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                      Erlandsson A., Holm P., Ullen A., Stigbrand T., Sundstrom B.E.; Studies of the interactions between the anticytokeratin 8 monoclonal antibody TSI, its antigen and its anti-idiotypic antibody alphaTSI."; Mol. Recognit. 16:157-163(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novotny J., Margolies M.N.; "Amino acid sequence of the light chain variable region from a mouse anti-digoxin hybridoma antibody."; Biochemistry 22:1153-1158(1983).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHV-PWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQTTHVPPYTFGGGTKLEMK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 115;
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Brlandsson A.;

Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.

EMBL, A1846475; CAI56337.1; -; mRNA.

InterPro; IPR003599; Ig.

InterPro; IPR003110; Ig-like.

InterPro; IPR003596; Ig v.

Fran, FF00686; V-set; I.

SMART; SM00406; IG; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 AA; 12560 MW; E4D3BF3D63E88007 CRC64;
                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.3%; Score 483.5; DB 2
81.4%; Pred. No. 1.3e-42;
iive 12; Mismatches 8
                                                                    10-MAY-2005 (TrEMBLrel. 30, Last sequence upda
10-MAY-2005 (TrEMBLrel. 30, Last annotation up
Kappa light chain variable region (Fragment).
Name-1gGl anti-TS1 VL;
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                                               Created)
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MEDLINE=83178921; PubMed=6404298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50835; IG LIKE; 1.
                                               10-MAY-2005 (TrEMBLrel. 30,
QSF210 MOUSE PRELIMINARY, QSF210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                 Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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TISSUE=Lung;
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                                                         This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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A Rlauener R.D., Collins P.S., Wagner L., Shemmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Marny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
  MISCELLANEOUS: This chain was isolated from an 1gG2a hybridoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGVPDRFSGSGSGTDFTLKISRVEAEDLGIYFCSQTTHVPPTFGGGTKLEIK 112
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                                                                                                                                                                                                                                                                                                                                           Hybridoma; Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                       Complementarity-determining-1. Framework-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complementarity-determining-3.
Pramework-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113
12273 MW; F9F39CE949A84C2A CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81.0%; Score 482; DB 1;
81.2%; Pred. No. 1.8e-42;
                                                                                                                                                                                                                                                                                                                                             Direct protein sequencing; Hybridoma; Immunos
Immunoglobulin V region; Monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         239 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Mismatches
                                                                                                                                                                                                            HSSP, Q99M37, 1191.
Ensembl, ENSMUSG00000055315, Mus musculus.
InterPro, IPR007110; Ig-like.
InterPro, IPR003596; Ig_v.
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                      protein that binds digoxin.
                                                                                                                                                                                                                                                                                                   SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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Q8TCDO;
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nes 91; Conservative
                                                                                                                                                                                          PIR; A01914; KVMS26.
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94
103
23
113 AA;
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SEQUENCE
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Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and intial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Klein R., Jaenichen R., Zachau H.G.; "Expressed human immunoglobulin kappa genes and their hypermutation."; Eur. J. Immunol. 23:3248-3262(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wagner S.D., Luzzatto L.; "V kappa gene segments rearranged in chronic lymphocytic leukemia are distributed over a large portion of the V kappa locus and do not show
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
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                                                                                                                                                                                                                                                                                                                                                                             PubMed=1598223;
Hizabayashi Y., Munakata Y., Sasaki T., Sano H.;
"Vaziable regions of a human anti-DNA antibody O-81 possessing lupus
nephritis-associated idiotype.";
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Laturner-Mateske A., Huber C., Meindl A., Pargent W., Schable K.F.,
Thiebe R., Zocher I., Zachau H.G.;
"The human immunoglobulin kappa locus. Characterization of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
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PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG WHC; UNKNOWN 1.
Hypotherical protein; Immunoglobulin domain.
SEQUENCE 239 AA; 26235 WW; FACEDC3A3B03871D CRC64;
                                                                                                                     and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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80.4%; Pred. No. 7.2e-42;
ive 13; Mismatches 9;
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EMBL; BC022362; AAH22362.1; -; mRNA.
PIR; S22658; S22658.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            nephritis-associated idiotype.";
Nucleic Acids Res. 20:2601-0(1992).
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Eur. J. Immunol. 22:1023-1029(1992)
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SMR; Q8TCD0; 21-237.
InterPro; IPR007110; 1g-like.
InterPro; IPR003597; 1g-c1.
InterPro; IPR003006; 1g-MHC.
InterPro; IPR003596; 1g-v.
Pfam; PP07654; C1-set; 1.
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; $40324; $40324.
; $40374; $40374.
; $42267; $42267.
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NUCLEOTIDE SEQUENCE.
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Q6PIH6 HUMAN
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Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Broak S.A., McKennan R.J., Macken R.D., Mullahy S.J.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska W.,
Beneration and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC063299; AAH63599.1; -; mRNA.
HSSP; P01837; 1KCU.
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SEQUENCE 239 AA; 26245 MW; CD7313DDFFD358B3 CRC64;
                                                                                        05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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80.4%; Pred. No. 9.1e-42;
                                                 239 AA
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INCEPTO: JPR003599; IG.
INCEPTO: JPR00310; IG-like.
INCEPTO: JPR00310; IG-L.
INCEPTO: JPR003006; IG-L.
INCEPTO: JPR003596; IG-N-C.
INCEPTO: JPR003596; IG-N-C.
PERM: SM00409; IG: 2.
SWART; SM00409; IG: 2.
SWART; SM00407; IG-L; I.
PROSITE; PS00290; IG-LIKE; 2.
PROSITE; PS00290; IG-MHC; UNKNOWN-I.
                                                 PRT;
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                                              QEP491_HUMAN PRELIMINARY;
Q6P491;
                                                                                                                                                                Hypothetical protein. Homo sapiens (Human).
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TISSUE=Skin;
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Best Local S:
Matches 90,
  RESULT 10
                           Q6P491
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TISSUE=Ling;

MEDLINE=2238825;

PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Rausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A physins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Backer M.J., Usdin T.B., Ponaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodersten B.J., Lu X., Gibbs R.A.,

Rahesley A., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Schnerfield YS.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerchion and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                   Created)
Last sequence update)
Last annotation update)
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                  240 AA.
            PRT;
                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
QEPIHE_HUMAN PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                          Name=IGKV1-5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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KV2A\_HUMAN

RESULT 11

RESULT 12

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219 AA;
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                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                               Fougereau M.;
Submitted (NO
                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                 Matches
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HSSP; P01751; INQB.
SMR; P01614; 2-115.
GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:00068555; P:immune response; NAS.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003196; Ig-v.
SMART; SM00406; IGv; 1.
BROGITE; PSSO3835; IG_LIKE; 1.
Immunoglobulin V region.
                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHS-NGWTYLQWYLQKPGQSPQLLIYKVSNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Muš. musculus (Moŭse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                "The complete amino acid sequence of Bence Jones protein Cum (kappa-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 LYGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 ASGVPDRFSGSGSGSTDFTLKISRVQAEDVGVYYCMQRLEIPYTFGQGTKLEIR 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 79.2%; Score 471.5; DB 1; Length Best Local Similarity 80.5%; Pred. No. 2.3e-41; Matches 91; Conservative 10; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 AA; 12676 MW; 59E9F90A379569EC CRC64;
                                                                                                                                                                                      Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
18 kappa chain V-II region Cum.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        By similarity.
                                                                                                                                                                                                            SEQUENCE REVISION TO 50; 52; 96 AND 97.
MEDLINE=70063440; Pubmed=4188189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                            MEDLINE=68242259; PubMed=5586923;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q53VP8 MOUSE PRELIMINARY;
Q53VP8;
  STANDARD;
                                                                                                           NCBI_TaxID=9606;
                                                                                                                                PROTEIN SEQUENCE.
                                                                                                                                                                                                                                    Hilschmann N.:
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KV2A HUMAN
P01614;
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SEQUENCE
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1D 055
AC 055
DT 133
DT 133
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OC Bull
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Kipp B., Schlaak M., Becker W.M.;
"Cloning and expression of a recombinant mouse Pab-fragment recognizing a defined linear epitope of Chironomus thummi thummi major allergen Chi t. I.";
Int. Arch. Allergy Immunol. 110:348-353(1996).
EMBL; 237499; (GA885724.1; -; mRNA.
SMR; Q65ZC0; 1-219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIVMIQSPLSLPVTPGEPASISCRSSQSIVHSNGNIYLQWYLQKPGQSPQLLIXKVSNRL
                                                                a germ-line network by paucigene encoded Ab2 (anti-idiotypic) antibodies in the GAT system.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Kappa light chain C region (Fragment).

Mus musculus (Mouse).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

MUCBI_TAXID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGIYYCPQGIHVPYTFGGGTRLEIK 112
NUCLEOTIDE SEQUENCE.
MEDINE=8613012; Pubed=3937730;
01lier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
"The idiotypic network and the internal image; possible regul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.2%; Score 471; DB 2; Length 112; 80.4%; Pred. No. 2.6e-41;
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                                                                                                                                                                                                                                                                                        (NOV-1986) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                         112 AA; 12266 MW; C844B7881A89C18A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78.5%; Score 467; DB 2; 79.5%; Pred. No. 1.5e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80.4%; Pred. No. Live tive 10; Mismatches
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STRAIN=Balb/c; TISSUE=Spleen;
MEDLINE=96319505; PubMed=8768802;
                                                                                                                                                                                                                                                                                                                    EMBL; X03386; CAA27113.1; -; mRNA.
NON TER 1
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InterPro; IPR003599; IG.
InterPro; IPR003597; IG-like.
InterPro; IPR003596; IG_MHC.
InterPro; IPR003596; IG_WHC.
InterPro; IPR003596; IG_V.
Pfam; PF07654; Cl-set; I.
SWART; SW00409; IG; 2.
SWART; SW00400; IG; 1.
SWART; SW00406; IGV; I.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS002509; IG_MHC; I.
                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE OF 108-109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23944 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QESZCO_MOUSE PRELIMINARY;
Q6SZCO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90; Conservative
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                                                                             1 ELVMIQSPLSLSVSLGDQASISCRSSQSLVHINGNIYLHWYLQKPGLSPKLLIYIVSNRF 60
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Riesen W.F., Jaton J.-C.;
"Variable region sequence of the light chain from a Waldenstroms IgM with specificity for phosphorylcholine.";
Blochemistry 15:3829-3831(1976).
-I- MISCELLANBOUS: This chain was isolated from a Waldenstrom's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
Gaps
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Complementarity-determining-3.
Framework-4.
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12; Indels
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PROSITE; PS50835; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               macroglobulin that binds phosphorylcholine.
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21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Imp kappa chain V-II region FR.
Homo sapiens (Human).
11; Mismatches
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89; Conservative
                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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102
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93
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61 SGVPDRPSDSGSGTDFTLKITRVQAEDVGVYYCMQATZSPYTFGQGTKLZIK 112
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Search completed: January 10, 2006, 20:53:25 Job time: 75.5025 secs

us-10-735-916a-65.rpr

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5.1.6
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 GenCore version (c) 1993 - 2006
            Copyright
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- protein search, using sw model OM protein Run on:

January 10, 2006, 20:28:02; Search time 13.5124 Seconds (without alignments) 797.508 Million cell updates/sec

1 DIVMTQSPLSLPVTPGEPAS......CFQGSHVPWTFGQGTKVEIK 112 US-10-735-916A-65 595 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB M

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES		
Result No.	Score	Query	Length	DB	ID		
	523	87.9	131	7	B39276	Ig light chain pr	pre
7	522	87.7	113	~	PL0203	ti-DNA autoan	q
٣	516	86.7	219	~	S52028		E
4	514	86.4	112	~	S58207	Ig light chain V	1 r
S	514	86.4	112	~	S38719	light	7
9	514	86.4	136	~	S40357	kappa chain	۷۲
7	513	86.2	112	~	A31807	kappa	7 1
8	513	86.2	219	~	PC4203	kappa chain	Ê
6	512	86.1	110	~	S26335	kappa chain	7 1
10	509	85.5	114	N	A32967	kappa chain	1-N
11	508	85.4	118	~	PT0359	kappa	, H
12	508	85.4	131	~	B34904	kappa chain	pre
13	206	85.0	112	~	B31485	kappa	/ r
14	504	84.7	112	~	C27887	kappa	/ r
15	504	84.7	131	7	C34904	kappa chain	pre
16	502	84.4	112	~	A27887	kappa	ı,
17	501	84.2	112	~	F27887	kappa	7 K
18	501	•	115	7	\$38715	kappa	7
19	501	84.2	132	~	S26882	chain V	/ r
20	200	•	114	~	B32967	kappa chain V	/-I
21	200		135	~	S40342	kappa	<u>ب</u>
22	499	83.9	112	~	E27887	kappa	/ r
23	499	83.9	117	-	KZHUGM	kappa chain	pre
24	499	•	131	7	B30577	kappa chain	pre
25	499	•	133	Н	K2HURP	kappa chain	pre
26	499	83.9	219	~	S16112	kappa	7 K
27	498	٠	103	N	PH1043	light	и /
28	498	83.7	131	~	D34904	kappa chain	pre
29	498	83.7	131	~	B32513	kappa chain	pre

	kappa kappa ibody	light kappa kappa	Ig kappa chain V r Ig kappa chain - h Ig kappa chain pre	light kappa kappa	kappa kappa
D28195 PL0257	A49715 S40339 S53750	B41940 S32189 JL0029	S22902 S40356 A24452	S58206 D27887 D29380	S23230 B27887
0.0	000	0 0 0	0 0 H	000	0 0
112	112 126 112	113 112 225	142 125 133	112	133
83.5	83.4 83.1 83.0	83.0 82.9 82.9	82.7 82.5 82.5	82.4 82.4 82.4	82.4 82.2
497 496	496 494.5 494	4 4 4 4 9 4 6 9 3	492 491 491	4 4 9 0 0 0 4 4 9 0	490 489
30	332 332 443	35 36 37	8 6 0 8 6 0	4 4 4 4 2 2 4 3	4 4 5

## ALIGNMENTS

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Ig light chain precursor V-D-J region (6-19) - mouse
[5] Species: Mus musculus (house mouse)
[6] Species: Mus musculus (house mouse)
[6] Species: Mus musculus (house mouse)
[7] Species: Mus musculus (house mouse)
[7] Species: Musculus (house mouse)
[7] Species: Musculus (house mouse)
[8] Species: Musculus (house mouse)
[8] R. Reininger, L.; Berney, T.; Shibata, T.; Spertini, F.; Merino, R.; Izui, S.

R. Reininger, L.; Berney, T.; Shibata, T.; Spertini, F.; Merino, R.; Izui, S.

R. Reininger, L.; Berney, T.; Shibata, T.; Spertini, F.; Merino, R.; Izui, S.

R. Reininger, Musculus (house)
R. Reference number: A39276; MulD:91088540; PMID:2263605
R. Residues: Dreliminary
R. Residues: 1-131 cREI
R. Residues: 1-131 cREI
R. Residues: 1-131 cREI
R. Residues: UNIPARC:UPI0000115153; GB:MS5313; NID:9198095; PIDN:AAA63385.1; PID
C. Superfamily: immunoglobulin V region; immunoglobulin homology cIMM>
F;35-114/Domain: immunoglobulin homology cIMM>
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Gapa ; 0 Query Match

87.9%; Score 523; DB 2; Length 131;
Best Local Similarity 86.6%; Pred. No. 2.1e-42;
Matches 97; Conservative 10; Mismatches 5; Indels

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DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60 -20 ઠે 셤

61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCPQGSHVPWTFGQGTKVEIK 112 80 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCPQGSHVPYTFGSGTKLEIK 131 à 셤

# RESULT 2

anti-DNA autoantibody BV17-31, kappa chain V region - mouse (fragment)
c;psecises: Mus musculus (house mouse)
c;psecises: Mus musculus (house mouse)
c;pacession: PL0203
R;Smith, R.G.; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1990
A;Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from NA;Reference number: PL0198; MUID:90309768; PMID:2114528

A; Molecule type: mRNA A; Residues: 1-113 <5M1.> A; Residues: 1-113 <5M1.> A; Cross-references: UNIPARC:UP10000113786; GB:X53643; NID:g50196; PIDN:CAA37694.1; PID:g C; Superfamily: immunoglobulin homology <1MM> F; 16-95/Domain: immunoglobulin homology <1MM> F; 16-95/Domain: immunoglobulin homology <1MM> F; 16-95/Begion: complementarity-determining 1 F; 16-102/Region: complementarity-determining 2 F; 101-113/Region: D region

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A;Residues: 1-112 <CIM>
A;Residues: 1-112 <CIM>
A;Cross-references: UNIPARC:UPI0000117543; EMBL:X76021; NID:9416112; PIDN:CAA53608.1; PL.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 31-Dec-2004
C;Accession: S40357
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: 840312; MUID:94080891; PMID:8258341
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Ig kappa chain V region (PAC1) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Jul-1989 #sequence_revision 20-Jul-1989 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                   Ig light chain V region - mouse
C;Species: Nus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C;Accession: S38719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DIVWIQTPLSLPVSLGDQASISCRSSQSIVYSNGNTYLEWYLQKPGQSPKLLIXKVSNRF
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61 YGVPDRFSGSGSGTDFTLKISRVEABDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                            61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPWTFGQGTKVEIK 112
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C;Superfamily: immunoglobulin homology
C;Keywords: heteroctetramer; immunoglobulin
F;36-115/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86.4%; Score 514; DB 2; Length 11 llarity 86.6%; Pred. No. 1.3e-41; Conservative 9; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             R_iCimanis, A.Y. submitted to the EMBL Data Library, November 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Reference number: S38713
A, Accession: S38719
A, Status: preliminary
A, Molecule type: mRNA
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Matches 97; Conserv
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8
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Ig kappa chain - mouse
C; Species: Mus musculus (house mouse)
C; Accession: 552028
R; Van Engelen, F.; Schouten, A.; Molthoff, J.W.; Roosien, J.; Dirkse, W.G.; Schots, A.; Submitted to the EMBL Data Library, August 1994
A; Description: Coordinate expression of antibody subunit genes yields high levels of fun A; Reference number: 552028
A; Accession: 552028
A; Cooser-references: UNIPARC: UPI0000114B22; EMBL: L35138; NID: G522336; PIDN: AAA67525.1; PIC; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 16-95/Domain: immunoglobulin homology <IMM>
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 21-Jan-2000
C;Accession: S58207
R;Welschof, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebel, S.; Breitling, submitted to the EMBL Data Library, July 1995
Appearription: Characterization of heavy and light chain immunoglobulin variable region A;Reference number: S58206
A;Accession: S58207
A;Accession: S58207
A;Accession: S58207
A;Accession: S58207
A;Accession: S68207
A;Accession: Marcession: Ma
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                                                                                                                                                                                                                                           DVVMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRF
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                                                                                                                 Gaps
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                                        Length 113;
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                                                                                                                 5; Indels
                                    87.7%; Score 522; DB 2;
86.6%; Pred. No. 2.3e-42;
iive 10; Mismatches 5;
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                                                                        Local Similarity 86.6%
les 97; Conservative
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Best Local S:
Matches 97
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Matches
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Query Match 85.4%; Score 508; DB 2; Length 118; Best Local Similarity 83.9%; Pred. No. 5e-41; Matches 94; Conservative 10; Mismatches 8; Indels
                                                                                                                                     Query Match
Best Local Similarity
Matches 95: Conserv
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Best Local Similarity
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Cybecies: Alloec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000
CyAccession: PC4203
R;Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.
Gene 173, 257-259, 1996
A;Title: Cloning and characterization of cDNAs coding for heavy and light chains of a mc
A;Reference number: PC4202; MUID:97082978; PMID:8964510
A;Reference number: PC4203
A;Accession: PC4203
A;Accession: PC4203
A;Accession: PC4203
A;Cross-references: UNIPARC:UPI00001157E4; GB:U29147; NID:g1594225; PIDN:AAC52821.1; PII
C;Comment: This protein is specific for human plasma apolipoprotein A-I of high-density
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;1-112/Domain: V region #status predicted <CRG>
F;113-219/Domain: C region #status predicted <CRG>
C; Accession: A31807
R; Taub, R.; Gould, R.J.; Garsky, V.M.; Ciccarone, T.M.; Hoxie, J.; Friedman, P.A.; Shatt
Billow, Chem. 254, 252-265, 1989
A; Title: A monoclonal antibody against the platelet fibrinogen receptor contains a seque
A; Reference number: A1807
A; Accession: A31807
A; Accession: A31807
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-112 < TAUP
A; Residues: 1-112 < TAUP
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Superfamily: immunoglobulin
F; 16-95/Domain: immunoglobulin homology < INM>
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: 826335
R;Stark, S.E.; Caton, A.J.
J; Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein A;Reference number: 826309; MUID:91341421; PMID:1908510
A;Accession: 826335
A;Accession: 826335
A;Accession: 826335
A;Accession: 826335
A;Retus: preliminary
A;Molecule type: mRNA
A;Residues: 1-110 <STA>
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    86.2%; Score 513; DB 2; Length 11
l Similarity 84.8%; Pred. No. 1.6e-41;
95; Conservative 12; Mismatches 5; Indels
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Best Local Similarity
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A;Cross-references: UNIPARC:UP10000115F78; EMBL:X59183; NID:g52314; PIDN:CAA41893.1; PIC C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;16-95/Domain: immunoglobulin homology <IMM>
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C;Species: Mus musculus (house mouse)
C;Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 21-Jan-2000
C;Accession: A32967
R;Levy, R.; Assulin, O.; Scherf, T.; Levitt, M.; Anglister, J.
R;Levy, R.; Assulin, D.; Scherf, T.; Levitt, M.; Anglister, J.
A;Title: Probing antibody diversity by 2D NMR: comparison of amino acid sequences, pred3
A;Reference number: A32967; MUID:90057406; PMID:2819059
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A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual trr-
A;Btatus: preliminary; nucleic acid sequence not shown; not compared with conceptual trr-
A;Residues: 1-114 <LEX>
A;Residues: 1-114 <LEX>
A;Cross-references: UNIPARC:UP10000114F5D; GB:W30481; NID:g197157; PIDN:AAA38935.1; PID
C;Superfamaily: immunoglobulin tomunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>
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C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
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A;Title: A novel class of anti-DNA antibodies identified in BALB/c mice. A;Reference number: PT0352; MUD:91108325; PMID:1988536
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                                                                                                                                                                                                      Length 110;
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C;Comment: This protein is an anti-double-stranded DNA antibody
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;19-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                  ch 86.1%; Score 512; DB 2; 1 Similarity 86.4%; Pred. No. 1.9e-41; 95; Conservative 10; Mismatches 5;
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Gaps

us-10-735-916a-65.rpr

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C;Accession: C27887
R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
A;Mo J. 5, 1577-1587, 1986
A;Title: Structural and functional implications of a restricted antibody response to a G.
A;Reference number: A91043; MUID:86300658; PMID:2427335
A;Accession: C27887
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Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cipate: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 09-Jul-2004
CiAccession: 034904; I31485
R;Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
A;Dil. Chem. 255, 133-138, 1990
A;Title: Active site structure and antigen binding properties of idiotypically cross-reamaly. R;Reference number: A34903; MUID:90094387; PMID:2104617
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A; Residues: 1-131 cBED>
A; Crose_references: UNIPROT: Q8VCI6; UNIPARC: UPI00001767A8
B; Crose_references: UNIPROT: Q8VCI6; UNIPARC: UPI0001767A8
B; Bedzyk, W-D: Johnson, L.S.; Riordan, G.S.; Voss Jr., E.W.
J. Biol. Chem. 264, 1565-1569, 1989
A; Title: Comparison of variable region primary structures within an anti-fluorescein idio
A; Reference number: A31485; MUID:89109167; PMID:2492278
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                                                          Ig kappa chain V region (H37-82) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
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                                                                                                                                                                                                                                                                                                                                                                                                   A;Experimental source: strain Balb/c
A;Experimental source: strain Balb/c
A;Note: this sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>
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C;Superfamily: immunoglobulin vegion; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;35-114/Domain: immunoglobulin homology <IMM>
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84.7%; Score 504; DB 2; Length 13
Best Local Similarity 83.0%; Pred. No. 1.3e-40;
Matches 93; Conservative 10; Mismatches 9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sest Local Similarity
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A; Residues: 1-112 < CAT>
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B31485
IG Wappa chain V region (4-4-20) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 09-Jul-2004
R;Bedzyk, W.D.; Johnson, L.S.; Riordan, G.S.; Voss Jr., E.W.
J; Biol. Chem. 264, 1565-1569, 1989
A;Till: Comparison of variable region primary structures within an anti-fluorescein idi
A;Reference number: A31485; MUID:89109167; PMID:2492278
A;Accession: B31485
A;Accession: bype: protein
A;Residues: 1-112 <br/>ABD>
A;Cross-references: UNIPROT:Q8VCI6; UNIPARC:UP10000176AF8
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <INM+>
                                                                                                                                                                                                                                                                     RESULT 12
B34904
Ig kappa chain precursor V region (12-40 and 5-14) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jul-2000
C;Accession: B34904, #134903
R;Bedzyk, W.D.; Herron, J.M.; Edmudson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A;Title: Active site structure and antigen binding properties of idiotypically cross-rea
A;Reference number: A34903; MUD:90094387; PMID:2104617
A;Accession: B34904
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRMA
A;Residues: 1-131 < RED>
A;Cross-references: UNIPARC:UPI0000114FC8; GB:M32384; GB:J05237; GB:J05238; NID:g639656;
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heteroterramer; immunoglobulin homology < IMM>
F;35-114/Domain: immunoglobulin homology < IMM>
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9
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   DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                   DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRF
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                                                                                                                          61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCPQGSHVPWTFGQGTKVEIK 112
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1 Similarity 83.9%; Pred. No. 5.6e-41;
94; Conservative 10; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.0%; Score 506; DB 2; Length 11 llarity 83.0%; Pred. No. 7.2e-41; Conservative 12; Mismatches 7; Indels
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		10n	Anti-IGF-	Human ant	Anti-IGF-		Anti-IGF-				Variable	_	Variable				•	Variable		Variable	_	•				Humanised
		Description	Adj76899	Adz67069	Adj 76901	Adz67071	Adj 76895	Adz67065	Adj 76897	Adz67067	Adp84950	Aae15713	Adp84948	Aae15712	Abp72125	Ade36495	Adp84946	Adp84951	Ade36530	Adp84949	Aae15711	Adp84944	Ade36523	Aay42960	Adp84947	Aay42969
SUMMARIES		ar	ADJ76899	ADZ67069	ADJ76901	ADZ67071	ADJ76895	ADZ67065	ADJ76897	ADZ67067	ADP84950	AAE15713	ADP84948	AAE15712	ABP72125	ADE36495	ADP84946	ADP84951	ADE36530	ADP84949	AAE15711	ADP84944	ADE36523	AAY42960	ADP84947	AAY42969
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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-1R) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-1R. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-1R and/or receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of

Disclosure; SEQ ID NO 65; 164pp; French.

Aar32239 Humanised	Aaw27145 Mature li	Aay87571 Humanised	Ade36522 Anti-FGF-	•		-		Adp84952 Variable			Adj80420 Hybrid hu	Adh61998 Human ant	Abr40268 Amino aci	Ade27687 Humanised	Ade36527 Anti-FGF-	Adj80422 Murine an	Adz52545 Anti-CCR4	Aea33234 CC chemok	Abr40272 Amino aci	Ade27694 Humanised
AAR32239	AAW27145	AAY87571	ADE36522	ADP84945	ABP72129	ADE36520	ADV67310	ADP84952	ADP84943	ADE36518	ADJ80420	ADH61998	ABR40268	ADE27687	ADE36527	ADJ80422	ADZ52545	AEA33234	ABR40272	ADE27694
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93.6	93.6	93.6	93.6	93.6	93.4	93.4	93.4	93.4	92.9	95.8	92.3	92.3	91.9	91.9	91.9	91.9	91.9	91.9	91.8	91.8
557	557	557	557	557	556	556	556	556	553	552	549	549	547	547	547	547	547	547	546	546
25	26	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	4	45

### ALIGNMENTS

ADJ76899

insulin-like growth factor-1 receptor; IGF-IR; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region; New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers. cytostatic; antipsoriatic; antibody; (FABR ) FABRE MEDICAMENT SA PIERRE. ADJ76899 standard; protein; 112 AA Anti-IGF-1R related protein #14. Leger O; 18-JAN-2002; 2002FR-0000653. 18-JAN-2002; 2002FR-0000654. 07-MAY-2002; 2002FR-0005753. 20-JAN-2003; 2003WO-FR000178. 06-MAY-2004 (first entry) Goetsch L, Corvaia N, WPI; 2003-569653/53 WO2003059951-A2. Homo sapiens. 24-JUL-2003. ADJ76899;  ~

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these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate. Jung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF. IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                  neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obsterincs; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder;
                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
                                                                                                                                                                1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                                                                                                                                                                      1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                        Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
                                                                                                                                                                                                              61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                Human antibody 7C10 2 light chain variable region SEQ ID NO:65.
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                                                                                                                     Length 112;
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                                                                                                                  100.0%; Score 595; DB 7;
100.0%; Pred. No. 2.5e-43;
iive 0; Mismatches 0;
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18-JAN-2002; 2002FR-0000554.

07-MAY-2002; 2002FR-0005753.

20-JAN-2003; 2003WO-FR000178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-DEC-2003; 2003US-00735916.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for treating cancer.
                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                          Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goetsch L, Corvaia N,
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CORVAIA N.
LEGER O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2005-321968/33
                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DUFLOS A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAEUW J.
                                                                                              Sequence 112 AA
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The invention relates to a novel isolated anti-insulin-like grow'n ractor capable of binding to human IGF-IR and, if necessary, capable of capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tyrosine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary comprising a light or heavy chain having at least one complementary comprising a light or heavy chain having at least one complementary comprising a light or heavy chain having at least one complementary comprising a light or heavy chain having at least one complementary comprising a light or heavy chain an attribody of the invention is useful in the preparation of a medicament intended for the prevention or treatment comprising of the IGF-IR and/or connected with a normal activation of the IGF-IR and/or connected with a cativation of the IGF-IR and/or of EGF with EGFR, where induces accordance of IGF-I or IGF2 with IGF-IR and/or of EGF with EGFR, where the administration of the medicament does not induces accordance of IGF-I or IGF2 with IGF-IR and/or of EGF-dependent and/or IGF2 dependent and/or EGF-dependent and/or IGF2-dependent and/or EGF-dependent and/or IGF2-dependent and/or IGF2-dependent and/or IGF2-dependent and/or IGF2-dependent and/or IGF2-dependent cells, preferency of a medicament intended for preparation of a medicament intended for prevention or for the reatment of cancer, where the cancer is chosen from prostate cancer, osteosarcoma lung cancer, breast cancer, endometrial cancer or colon cancer. (I) is useful in preparation of a medicament intended for the prevention or for the reatment of psoriasis. (I) is useful in preparation of a medicament intended for the prevention or colon cancer. (I) is useful in preparation of a medicament intended for the prevention or colon cancer. (I) is useful in the special or an underexpression of the IGF-IR and/or EGFR receptor is useful for in vitro diagnosis of a biologically and/or EGFR receptor is useful in the exemplificatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
relates to a novel isolated anti-insulin-like growth factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIVMTOSPLSLPVTPGEPASISCRSSOSIVHSNGNTYLOWYLOKPGOSPOLLIYKVSNRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic; antipsoriatic; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-IGP-1R related protein #15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADJ76901 standard; protein; 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-MAY-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003059951-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADJ76901;
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(i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (IGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit prowth and/or proliferation of tumor cells, so are useful against cancers of the proliferation from the indicative and or also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79
                                                                                                                                                                                                          New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQWYLQKPGQSPQLLIXKVSNRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DIVMTOSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGOSPQLLIYKVSNRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYCPQGSHVPWTFGQGTKVBIK 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 595; DB 7; Length 131; 100.0%; Pred. No. 3e-43; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein sequence used to generate the Ab of the invention
                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 67; 164pp; French

    19
    note= "leader peptide"

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                                                                                                      (FABR ) FABRE MEDICAMENT SA PIERRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADZ67071 standard; protein; 131 AA
                                                                                                                                        Goetsch L, Corvaia N, Leger O;
                                  18-JAN-2002; 2002FR-00000653.
18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
 20-JAN-2003; 2003WO-FR000178.
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Matches 112; Conservative
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                                                                                                                                                                           WPI; 2003-569653/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 131 AA;
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The invention relates to a novel isolated anti-insulin-like growth factor

I receptor (IGF-IR) antibody (I) or its functional fragment, being
capable of binding to human IGF-IR and, if necessary, capable of
specifically inhibiting tyrosine kinase activity of the receptor,
comprising a light or heavy chain having at least one complementary
determining region (CDR) consisting of one of two fully defined 16 amino
acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in
the preparation of a medicament intended for the prevention or treatment
of an illness connected with an overexpression and/or an abnormal
contineation of the IGF-IR and/or EGFR, and/or connected with a connected with a charaction of the irransduction pathway of the signal mediated by the
interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where
the administration of the medicament does not induce or only slightly
induces secondary effects connected with inhibition of the insulin
receptor. The antibody is useful for preparation of a medicament intended
to inhibit the transformation of normal cells into cells with tumoral
conserter, preferably IGF-dependent, especially IGF1 and/or IGF2-dependent
and/or Heppendent and/or EGF-dependent and/o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (I), which is optionally labeled. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) artibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the cancer is chosen from prostate cancer, osteosarcoma, lung cancer, breast cancer, endometrial cancer or colon cancer. (I) is useful in the preparation of a medicament intended for the prevention or for the treatment of psoriasis. (I) is useful in preparation of a medicament intended for the specific targeting of a biologically active compound to cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I) is useful for in vitro diagnosis of illnesses induced by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ä
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74. .80
/note= "CDR2"
                                                                                                                                        /note= "CDR3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WO-FR000178.
11-JUL-2003; 2003FR-00008538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2002FR-00000653
                                                                                                                                                                                                                                                                                                                                                                                                                                    16-DEC-2003; 2003US-00735916
                                                                                      113. .121
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CORVAIA N.
LEGER O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DUFLOS A. HAEUW J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ADZ67070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-JAN-2002;
                                                                                                                                                                                                                                                                                                                                    21-APR-2005
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(HAEU/)
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     Region
                                                                                                     Region
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Sequence 131 AA;

/note= "CDR1"

Region

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Gaps

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0; Indels

Mismatches

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111; Conservative

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic, antipsoriatic; antibody; IGF-IR; tyrosine kinase activity; insulin-like growth factor-1 receptor; IGFR; signal transduction pathway; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                 DIVMIQSPLSLPVIPGEPASISCRSSQSIVHSNGNIYLQWYLQKPGQSPQLLIXKVSNRL
                                                                                        DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                                   Gaps
                                                                                                                                                               61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                    80 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 131
                                                   ;
0
               Length 131;
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                                                   Indels
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               Score 595; DB 9;
Pred. No. 3e-43;
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Pred. No. 3.1e-43;
       100.0%; Score 5.2, 100.0%; Pred, No. 3e-43; +ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 61; 164pp; French
                                                                                                                                                                                                                                                                                              ADJ76895 standard; protein; 112 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (FABR ) FABRE MEDICAMENT SA PIERRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goetsch L, Corvaia N, Leger O;
                                                                                                                                                                                                                                                                                                                                                                                                         Anti-IGF-1R related protein #12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JAN-2002; 2002FR-00000653.
18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
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                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                Best Local Similarity 100.
Matches 112; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003059951-A2
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                                                                                        Н
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               Query Match
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Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lump tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinom; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGP-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                         1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                                   YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                        Human antibody 7C10 1 light chain variable region SEQ ID NO:61.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 12; SEQ ID NO 61; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                   cocation/Qualifiers
                                                                                                                                              Ā
                                                                                                                                             ADZ67065 standard; protein; 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002FR-00000653.
2002FR-00000654.
2002FR-00005753.
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/note= "CDR1"
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94. .102
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/note= "CDR3"
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                                                                                                                                                                                                                                                                                                                               chain variable region.
                                                                                                                                                                                                 entry)
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CORVAIA N.
LEGER O.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2005084906-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-MAY-2002;
20-JAN-2003;
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                       ADZ67065;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (DUFL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HAEU/)
                                                                                                                                                                                                                                                                                                                                                                                                 Region
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                                                                                                                                                                                                                                                                                                                                                                                    Key
                                                                                                                      RESULT 6
                                                                                                                                 ADZ67065
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determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of the preparation of the IGP-IR and/or Connected with a activation of the IGP-IR and/or EGFR, and/or connected with a cativation of the IGP-IR and/or EGFR, and/or connected with a cativation of the IGP-IR and/or EGFR, where the administration of the readdednent does not induce or only slightly induces secondary effects connected with inhibition of the insulin creeptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral character, preferably IGP-dependent, especially IGF1 and/or IGF2-dependent and/or HER2/neu-dependent cells. [I] is useful for preparation of a medicament intended to inhibit the proliferation of tumor cells, preferably IGP-dependent.

CC HER2/neu-dependent cells. [I] is useful in the preparation of a medicament intended for prevention or for the treatment of sories, leaded for prevention or for the treatment of cancer, endometrial cancer or colon cancer. [I] is useful in the preparation of a medicament intended for prevention or for the prevention of a medicament intended for prevention or for the prevention of a medicament intended for prevention or for the prevention or a medicament colls. [I] is useful in preparation of a medicament intended for prevention or for the prevention of a medicament intended for prevention or for the prevention or content of medicament content intended for prevention or for the prevention of a medicament intended for prevention or for the prevention of a medicament intended for prevention or for the prevention of a medicament intended for the specific targeting of a biologically active compound to calls expressing or overexpressing of illnesses induced by an expressing or overexpressing of illnesses induced by an expressing or overexpressing or the prevention of the pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (I), which is optionally labeled. The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
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  specifically inhibiting tyrosine kinase activity of the receptor,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.8%; Score 594; DB 9; Length 112; 99.1%; Pred. No. 3.1e-43; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence is used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADJ76897 standard; protein; 131 AA
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Matches 111; Conservative
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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or creat diseases associated with overexpression and/or abnormal activity of IGF-IR. Ab and its fragments are used to prevent or IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointesinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 79
                                                                                                                                                                 New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 594; DB 7; Length 131;
Pred. No. 3.6e-43;
1; Mismatches 0; Indels
                                                                                                                                                                                                                        Disclosure; SEQ ID NO 63; 164pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "leader peptide"
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                                                      (FABR ) FABRE MEDICAMENT SA PIERRE.
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                                                                                           Leger 0;
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/note= "CDR1"
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18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-00005753.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.8%;
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Matches 111; Conservative
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                                                                                           Corvaia N,
                                                                                                                            WPI; 2003-569653/53.
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/note= "CDR3"

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Treeptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of capable of binding to human IGF-IR and, if necessary, capable of eapable of binding to human IGF-IR and, if necessary, capable of capable of binding tyoshine kinase activity of the receptor, capable of ADZ670141 and antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or of EGF with EGFR, where the administration of the transduction pathway of the signal mediated by the interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly induced by the interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly creeptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral character, preferably IGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or IGF2-dependent and/or IGF2-dependent and/or EGF-dependent and/or EGF-depe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel isolated anti-insulin-like growth factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
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                                                                                                                                                                                                2002FR-00000654.
2002FR-00005753.
                                                                                                                                                                              2002FR-00000653
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11-JUL-2003; 2003FR-00008538.
                                                                                                                               16-DEC-2003; 2003US-00735916
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CORVAIA N.
LEGER O.
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                                            US2005084906-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                               BECK A.
                                                                                                                                                                              18-JAN-2002;
                                                                                                                                                                                                                          07-MAY-2002;
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                                                                                        21-APR-2005
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(HAEU/)
(BECK/)
                                                                                                                                                                                                                                                                                                                                       (CORV/)
(LEGE/)
                                                                                                                                                                                                                                                                                                                (GOET/)
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Score 594; DB 9; Pred. No. 3.6e-43; 99.8%; Query Match Best Local Similarity

Length 131;

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This invention describes novel recognition molecules, especially antibodies that bind specifically to the Core-1 antigen. The recognition molecules are used to make constructs containing the framework regions that separate, include and/or flank the specified sequences, especially where the framework regions are from the immunoglobulin (Ig) superfamily, protease inhibitors. Lectims, helix-bundle proteins and/or lipocalins. Most especially the framework regions are from antibodies, particularly the variable heavy chain (WH) and the variable light chain (VL) of human and/or murine origin. The constructs may also include a His or myc tag, a lysine-rich region and/or a multimerisation domain, most particularly it is a single-chain antibody fragment, multibody, Fab fragment, fusion protein of an antibody fragment with peptide or protein, and/or an Ig of types G, M, A, E or D and/or their subclasses. It may be human, the humanised, murine or chimeric, e.g. IgM without the J chain. The additional sequences/structures in the constructs are Ig domains of various species, interacting or stabilising domains, signal sequences, fluorescent dyes, toxins, antibodies with catalytic activity or other specificities so cytolytic agents, enzymes, immuno-modulators or effectors, MHC molecules, antigens, chelators for radioactive labels, liposomes, transmembrane domains, viruses and/or cells, specifically
                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New recognition molecules, e.g. antibodies (and nucleic acids) that bind specifically to Core-1 antigens, useful for diagnosis, treatment and prevention of tumors and metastases.
                                                                                79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protease inhibitor; lectin; helix-bundle protein; lipocalin; diagnosis; variable heavy chain; VH; variable light chain; VL; vaccine; diagnosis; alleviation; treatment; tumour; breast; colon; stomach; pancreas; large/small intestine; ovary; cervix; lung; prostate; kidney; liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibody; Core-1 antigen; framework region; immunoglobulin superfamily;
                                                                                20 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                        1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
Gaps
                                                                                                                             YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFOGSHVPWTFGOGTKVEIK 112
                                                                                                                                                 80 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVBIK 131
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0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            Variable light chain VL fragment Karo24 SEQ ID NO 92.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stahn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Danielczyk A, Karsten U, Ravn P,
1, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NEMO-) NEMOD BIOTHERAPEUTICS GMBH & CO KG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 15; SEQ ID NO 92; 136pp; German.
                                                                                                                                                                                                                                                                              ADP84950 standard; protein; 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2003; 2003WO-DE003994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-NOV-2002; 2002DE-01056900
                                                                                                                                                                                                                                                                                                                                                                    09-SEP-2004 (first entry)
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-461095/43.
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Christensen PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Chimeric.
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                                                                                                                                                                                                                                                                                                                           ADP84950;
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                                                                                                                                                                                                                                      RESULT 9
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(SCAN-) SCANCELL LTD.

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          acid encoding them, and related vectors and host cells, are useful for prevention (e.g. as vaccine), diagnosis, alleviation, treatment, monitoring and/or secondary treatment of tumours (specifically of breast, colon, stomach, pancreas, large/small intestine, ovary, cervix, lung, prostate, kidney and/or liver) and/or metastases (particularly to liver), specifically where these are positive for the Ci antigen. The products of the invention provide simple, reliable and efficient detection of tumours. They are specific for carcinoma and show almost no binding to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse; humanised form; monoclonal antibody alpha 340; gene therapy; epidermal growth factor receptor; EGF; cancer; colorectal; lung; breast; gastric; ovarian; immune response; cytostatic; cell growth; apoptosis; inhibitor; mutant; mutein; variant.
                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                               1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLEWYLQKPGQSPQLLIYKVSNRF 60
                                                                                                                                                                                                                                                                               1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
macrophages. The antibodies, also constructs containing them, nucleic
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                   61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                 61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPYTFGQGTRVEIK 112
                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse monoclonal antibody alpha 340 Vk region variant, 340VKd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "Wild type Thr substituted with Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Wild type Asn substituted with Lys"
                                                                                                                                                                                                            Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "Wild type Asp substituted with Glu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "Wild type Gln substituted with Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "Wild type Leu substituted with Val"
                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "Wild type Ser substituted with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "Wild type Leu substituted with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "Wild type Lys substituted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "Wild type Leu substituted
                                                                                                                                                                                                           Score 570; DB 8;
Pred. No. 3.5e-41;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE15713 standard; protein; 112 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-MAY-2000; 2000GB-00011981.
24-AUG-2000; 2000GB-00020794.
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                                                                                                                                                                                                              Query Match
Best Local Similarity 96.4%;
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                               Sequence 114 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
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                                                                                                                                                 healthy tissue.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus sp.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE15713;
                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
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The present invention relates to a humanised form of the antibody 340 (a mouse monoclonal antibody which binds to epidermal growth factor (EGF) creceptor and inhibite binding of EGF), obtainable from the cell line deposited with the ECACC under accession number 97021428. The humanised form of the antibody 340 is useful in gene therapy, medicine and in the cinvention is useful for treatment or prophlaxis of cancer. The invention is useful for treating colorectal, lung, breast, gastric or ovarian cancers or also for preventing the recurrence of cancer after initial treatment or surgery. The invention is also useful for enhancing captures of a protective immune against cancer by optimised immunisation cabedules. The humanised form of the antibody 340 has reduced immunisation is thibbit the growth of EGF receptor expressing CCI receptor, as the original mutine antibody and has increased ability to inhibit the growth and apoptosis inhibitor. The present sequence is conservation antibody all phase of light chain variable (VK)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                   New humanized form of mouse monoclonal antibody 340 which binds to epidermal growth factor receptor and inhibits binding of growth factor, useful for treating colorectal, lung, breast, gastric and ovarian cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibody; Core-1 antigen; framework region; immunoglobulin superfamily; procease inhibitor; lectin; helix-bundle protein; lipocalin; variable heavy chain; VI; varcine; diagnosis; alleviation; treatment; tunour; breast; colon; stomach; panoreas; large/small intestine; ovary; cervix; lung; prostate; kidney; liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGIYYCFQGSHVPWTFGGGTKVEIK 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 567; DB 5; Length 112; Pred. No. 6.3e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Variable light chain VL fragment Karoll SEQ ID NO 90.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADP84948 standard; protein; 114 AA.
                                                                                                                                                                              Example 2; Fig 7; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2003; 2003WO-DE003994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 105; Conservative
                                 Durrant LG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 region variant, 340VKd
                                                                     WPI; 2002-062384/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2004050707-A2
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Chimeric.
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                                 Ellis JRM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADP84948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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inhibitor; mutant; mutein; variant.

Mus sp. Synthetic. Mus

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This invention describes novel recognition molecules, especially antibodies that bind specifically to the Core-1 antigen. The recognition completed is at the constructs containing the framework regions that separate, include and/or flamk the specified sequences, especially where the framework regions are from the immunoglobulin (Ig) superfamily, protease inhibitors: lectins, helix-bundle proteins and/or lipocalins. Most especially the framework regions are from antibodies, particularly the variable heavy chain (WH) and the variable light chain (VL) of human and/or murine origin. The constructs may also include a His or myc tag, a construct or more particularly it is a single-chain antibody fragment, multibody, Fab fragment, fusion (Vr) and antibody fragment with peptide or protein, and/or an Ig of types G, M, A, E or D and/or their subclasses. It may be human, the constructs are Ig domains of various species, interacting or stabilising domains of various species, toxins, antibodies with catalytic activity or other effectors, MHC molecules, antigens, chellising domains, signal sequences, consecuted and or protein edgents, and or antibodies with catalytic activity or other effectors. MHC molecules, antigens, chellators for radioactive labels, conference or protein or hard and related and hort cells, specifically and or completes. The antibodies will be containing them, nucleated and and hort chain and hort call are and hort cells, and hortors and hort cells, and hortors and hort cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acid encoding them, and related vectors and host cells, are useful for prevention (e.g. as vaccine), diagnosis, alleviation, treatment, monitoring and/or secondary treatment of tumours (specifically of breast, colon, stomach, pancreas, large/small intestine, ovary, cervix, lung, prostate, kidney and/or liver) and/or metastases (particularly to liver), specifically where these are positive for the C1 antigen. The products of the invention provide simple, reliable and efficient detection of tumours. They are specific for carcinoma and show almost no binding to
                                                                                                                                                                                                                        recognition molecules, e.g. antibodies (and nucleic acids) that bind cifically to Core-1 antigens, useful for diagnosis, treatment and
                                                                                    Stahn R;
                                                                                 Danielczyk A, Karsten U, Ravn P,
                          (NEMO-) NEMOD BIOTHERAPEUTICS GMBH & CO KG.
                                                                                                                                                                                                                                                                                                                                       Claim 15; SEQ ID NO 90; 136pp; German.
                                                                                                                                                                                                                                                        specifically to Core-1 antigens, usef
prevention of tumors and metastases.
                                                                                                                                                                WPI; 2004-461095/43.
                                                                                                              Christensen PA;
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                                                                                    Goletz S,
                                                                                                                                                                                                                             New
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ô 1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60 9 1 DIVMIQSPLSLPVIPGEPASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIXKVSNRF 0; Gaps 61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVBIK 112 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPYTFGQGTKVEIK 112 Score 566; DB 8; Length 114; Pred. No. 7.8e-41; 3; Mismatches 2; Indels 95.1%; Query Match
Best Local Similarity 95.55
Matches 107; Conservative ሯ 셤 ઠે 셤

Sequence 114 AA;

Mouse; humanised form; monoclonal antibody alpha 340; gene therapy; epidermal growth factor receptor; EGF; cancer; colorectal; lung; breast; gastric; ovarian; immune response; cytostatic; cell growth; apoptosis; Mouse monoclonal antibody alpha 340 Vk region variant, 340VKc. AAE15712 standard; protein; 112 AA. (first entry) 12-MAR-2002 AAE15712; AAE15712 

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Gaps

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1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60

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Query Match 94.8%; Score 564; DB 5; Length 112; Best Local Similarity 93.8%; Pred. No. 1.1e-40; Matches 105; Conservative 3; Mismatches 4; Indels

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The present invention relates to a humanised form of the antibody 340 (a mouse monoclonal antibody which binds to epidermal growth factor (EGF) receptor and inhibits binding of EGF), obtainable from the cell line edposited with the ECACC under accession number 97021428. The humanised form of the antibody 340 is useful in gene therapy, medicine and in the manufacture of a medicament for treatment or prophylaxis of cancer. The manufacture of a medicament for treatment or prophylaxis of cancer. The invention is useful for preventing the recurrence of cancer after ovarian cancers or also for preventing the recurrence of cancer after initial treatment or surgery. The invention is also useful for enhancing contective immune response against cancer by optimised immunisation schedules. The humanised form of the antibody 340 has reduced immune the present of the antibody 340 has reduced immune the properties of the antibody and has increased ability to receptor, as the original murine antibody and has increased ability to inhibit the growth of EGF receptor expressing cells. The invention is used as cell growth and apoptosis inhibitor. The present sequence is used as cell growth and apoptosis inhibitor. The present sequence is used as cell growth and apoptosis inhibitor. The present sequence is region variant, 340VKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New humanized form of mouse monoclonal antibody 340 which binds to epidermal growth factor receptor and inhibits binding of growth factor, useful for treating colorectal, lung, breast, gastric and ovarian cancer.
                                                                                                                                        note= "Wild type Thr substituted with Ser"
                                                                                                                                                                              note= "Wild type Ser substituted with Thr"
                                                                                                                                                                                                                     note= "Wild type Leu substituted with Pro"
                                                                                                                                                                                                                                                          note= "Wild type Asp substituted with Glu"
                                                                                                                                                                                                                                                                                                  note= "Wild type Gln substituted with Pro"
                                                                                                                                                                                                                                                                                                                                                                             note= "Wild type Leu substituted with Thr"
                                                                                                                                                                                                                                                                                                                                                                                                                      note= "Wild type Ile substituted with Val"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "Wild type Leu substituted with Val"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Wild type Asn substituted with Lys"
                                                                                                                                                                                                                                                                                                                                       note= "Wild type Lys substituted with
                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-MAY-2000; 2000GB-00011981.
24-AUG-2000; 2000GB-00020794.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Durrant LG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference 112
                                                                                                                                                                                                  Misc-difference 15
                                                                                                                                                                                                                                                                               Misc-difference 18
                                                                                                                                                                                                                                                                                                                       Misc-difference 50
                                                                                                                                                           Misc-difference 14
                                                                                                                                                                                                                                          Misc-difference 17
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                                                                                                                      Misc-difference
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Uchii M,
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                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                      Sequence 112 AA;
                                                               WO2003057251-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2004050707-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                             Unidentified
                                                                                  17-JUL-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        metastasis.
                                                                                                                                                           Tamura T,
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                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to novel humanised antibodies and antibody fragments which react with fibroblast growth factor 8 (FGF8) and inhibit its biological functions. The polypeptides of the invention have cytostatic activity. The antibody is useful for the treatment of cancer, including prostate, breast, ovarian and testicular cancer. The present sequence is used in the exemplification of the invention
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Anti-FGF-8 (sic fibroblast growth factor) antibody-related protein #2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                Humanised antibodies and antibody fragments reacting with fibroblast growth factor 8 useful for the treatment and diagnosis of cancer.
                                                                                                                                                                 Humanised; antibody; fibroblast growth factor 8; FGF8; cytostatic; cancer; prostate; breast; ovarian; testicular.
                           61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCPQGSHVPYTFGQGTKVEIK 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 112;
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Pred. No. 1.1e-40;
4; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                             Hirota M,
                                                                                                                                                                                                                                                                                                                                                                            Claim 19; Page 72; 86pp; Japanese.
                                                                                            ABP72125 standard; protein; 112
                                                                                                                                                  FGF-8 related protein SEQ ID 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADE36495 standard; protein; 112
                                                                                                                                                                                                                                                      28-JUN-2002; 2002WO-JP006591.
                                                                                                                                                                                                                                                                        28-JUN-2001; 2001JP-00196176,
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                                                                                                                                                                                                                                                                                          (KYOW ) KYOWA HAKKO KOGYO KK
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Best Local Similarity 94.6
Matches 106; Conservative
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                                                                                                                               03-JUN-2003
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1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention comprises a method for treating and preventing arthritis, the method involves the use of anti-FGF-8 (sic fibroblast growth factor) antibody. The antibody and method of the invention is useful for: the detection, treatment and prevention of arthritis; as a cartilage protection agent; as a joint destruction inhibitor; and as a synoviral proliferation inhibitor. The present amino acid sequence represents a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibody; Core-1 antigen; framework region; immunoglobulin superfamily; procease inhibitor; lectin; helix-bundle protein; lipocalin; variable heavy chain; VI; varcine; diagnosis; alleviation; treatment; tumour; breast; colon; stomach; panoreas; large/small intestine; ovary; cervix; lung; prostate; kidney; liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   comprising the use of anti-FGF-8
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94.6%; Pred. No. 1.1e-40;
ive 4; Mismatches 2; Indels
arthritis; anti-FGF-8; sic fibroblast growth factor; cartilage protection agent; joint destruction inhibitor; symoviral proliferation inhibitor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treatment and prevention of arthritis co (sic fibroblast growth factor) antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11, SEQ ID NO 19; 193pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Suda T, Miki I,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-DEC-2001; 2001JP-00400677
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This invention describes novel recognition molecules, especially antibodies that bind specifically to the Core-1 antigen. The recognition concletules are used to make constructs containing the framework regions are from the immunoglobulin (1g) superfamily, where the framework regions are from the immunoglobulin (1g) superfamily. Constructs are from antibodies, particularly the variable heavy chain (14) and the variable light chain (11) funmandor multimerisation domain, most particularly the variable heavy chain (14) and the variable light chain (11) of human and/or murine origin. The constructs may also include a His or myc tag, a lysine-rich region and/or amultimerisation domain, most particularly it is a single-chain antibody fragment, multibody, Fab fragment, fusion protein of an antibody fragment with peptide or protein, and/or an Ig of types G, M, A, E or D and/or their subclasses. It may be human, conversed, murine or chimeric, e.g. IgM without the J chain. The additional sequences/structures in the constructs are Ig domains of additional sequences/structures in the constructs are Ig domains of specific ities, cytolytic agents, enarymes, immuno-modulators or specificities, cytolytic agents, enarymes, immuno-modulators or effectors, MHC molecules, antibodies with catalytic activity or other specificities, cytolytic agents, enarymes, immuno-modulators or effectors, MHC molecules, antipodies with catalytic activity or other specification them, and related vectors and host cells, are useful for crevenancy them and or secondary treatment of tumours (specifically of parcens, lange and/or metastases (particularly to liver), colon, stomach, pancreas, large/small intestine, ovary, cervix, lung, prostate, kidney and/or simple, reliable and efficient detection of the invention provide simple, reliable and efficient detection of the linear or provide simple.
                                                                                                                                                                                                                                                                                                         New recognition molecules, e.g. antibodies (and nucleic acids) that bind specifically to Core-1 antigens, useful for diagnosis, treatment and
                                                                                                                                                                            Danielczyk A, Karsten U, Ravn P, Stahn R;
                                                                                                                          (NEMO-) NEMOD BIOTHERAPEUTICS GMBH & CO KG
                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 15; SEQ ID NO 88; 136pp; German
                                                                                                                                                                                                                                                                                                                                                            prevention of tumors and metastases.
                       01-DEC-2003; 2003WO-DE003994.
                                                                          29-NOV-2002; 2002DE-01056900
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                                                                                                                                                                            Goletz S, Danie
Christensen PA;
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Sequence 114 AA;

1 DIVMTOSPLSLPVTPGEPASISCRSSOSIVHSNGNTYLOWYLOKPGOSPOLLIYKVSNRL 60 1 DIQMIQSPLSLPVIPGEPASISCRSSQSIVHSNGNIYLEWYLQXPGQSPQLLIYKVSNRF 60 0; Gaps 94.8%; Score 564; DB 8; Length 114; 95.5%; Pred. No. 1.2e-40; ive 2; Mismatches 3; Indels Query Match Best Local Similarity 95.5' Matches 107; Conservative a ઠે

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1 DVVMTQSPLSLPVTPGEPAS.......CFQGSHVPWTFGQGTKVEIK 112
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Copyright (c) 1993 - 2006 Compugen Ltd
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TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
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PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-07-07
PRIOR FILING DATE: 2003-01-20
PRIOR FILING DATE: 2002-01-18
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100.0%; Pred. No. 2.5e-40;
iive 0; Mismatches 0;
US-10-932-334-86
US-10-932-334-90
US-10-932-334-90
US-10-512-184-65
US-10-512-184-66
US-10-512-184-66
US-10-932-334-10
US-10-932-334-11
US-10-932-334-84
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US-10-932-334-82
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Publication No. US20050249730A1
GENERAL INFORMATION:
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SEQ ID NO 67
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US-11-012-333-63

Sequence 63, Application US/11012353

Publication No. US20050249730A1

GENERAL INFORMATION:
APPLICANT GOETSCH, LILIANE
APPLICANT CORYALA, NATHALIE
APPLICANT CORYALA, NATHALIE
APPLICANT HAEUW, JEAN-FRANCOIS
APPLICANT HAEUW, JEAN-FRANCOIS
APPLICANT HAEUW, JEAN-FRANCOIS
APPLICANT HAEUW, JEAN-FRANCOIS
APPLICANT EBCK, OLIVIER
TITLE OF INVENTION: NOVEE ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEEPONE ANTIHODIES AND USES THEREOF
FILE REFERENCE: 017753-198
CURRENT APPLICATION NUMBER: P8 2004-12-16
PRIOR APPLICATION NUMBER: P7 2003-12-16
PRIOR PLING DATE: 2003-12-16
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-01-20
PRIOR PLING DATE: 2003-01-20
PRIOR FILING DATE: 2003-01-20
PRIOR PLING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
SPRIOR FILING DATE: 2002-01-18
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Publication No. US2005049730A1

GENERAL INFORMATION:
APPLICANT: OGERSCH, LILLARE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
APPLICANT: BLGER, OLIVIER
APPLICANT: BECK, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION NUMBER: US/11/012,353
CURRENT FILING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: PR 0308538
PRIOR APPLICATION NUMBER: PCT/FR03/00178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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GENERAL INCOCRATION

APPLICANT: GOGVAIA, NATHALIB

APPLICANT: CORVAIA, NATHALIB

APPLICANT: CORVAIA, NATHALIB

APPLICANT: DUFICOS, ALAIN

APPLICANT: HASUW, JEAN-FRANCOIS

APPLICANT: BECK, ALAIN

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

FILE REFERENCE: 01753-198

CURRENT FILING DATE: 2004-12-16

PRIOR APPLICATION NUMBER: 10/735,916

PRIOR PLILING DATE: 2003-07-11

PRIOR PLILING DATE: 2003-07-11

PRIOR PLILING DATE: 2003-07-11

PRIOR PLILING DATE: 2002-05-07

PRIOR PLILING DATE: 2002-06-07

PRIOR PLILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18
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PRIOR FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: FR 0200653
PRIOR PILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 0200654
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SEQ ID NO 65
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SOFTWARE: Patentin Ver. 3.3
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US-11-012-353-67
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CORGANISM: Homo sapiens
US-11-012-353-65
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SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSLLPWTFGQGTKVEIK 112
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                                                                                                                                                                                      TAPLICANT: KYONA HAKKO KOGYO CO., LTD.
TITLE OF INVENTION: CCR4-specific antibody composition
FILE REPRENCE: 249-363
CURRENT APPLICATION NUMBER: US/10/959,310
CURRENT FILING DATE: 2004-10-07
FRIOR APPLICATION NUMBER: US 60/572,784
FRIOR APPLICATION NUMBER: US 60/572,784
FRIOR APPLICATION NUMBER: US 60/572,784
FRIOR FILING DATE: 2004-10-08
FRIOR FILING DATE: 2004-16-21
NUMBER OF SEQ 1D NOS: 46
SOFTWARE: PATENTIN Ver. 2.1
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A APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
TITLE OF INVEXTION: CCR4-specific antibody composition; FILE REFERENCE: 249-363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 544; DB 6;
Pred. No. 2.2e-36;
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91.1%; Pred. No. ...
6; Mismatches
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CURRENT FILING DATE: 2004-10-07
PRIOR APPLICATION NUMBER: UP 2003-350162
PRIOR FILING DATE: 2003-10-08
PRIOR APPLICATION NUMBER: US 60/572,784
PRIOR FILING DATE: 2004-05-21
NUMBER OF SEQ ID NOS: 46
SEQ ID NO 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Synthetic peptide US-10-959-310-35
                                                                                                    US-10-959-310-35; sequence 35, Application US/10959310; Publication No. US20050287138A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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Matches 102, Conservative
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Matches 101; Conservative
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Pred. No. 1.6e-36;
6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 91.9%; Score 547; DB 6; Length 112; Best Local Similarity 92.0%; Pred. No. 1.3e-36; Matches 103; Conservative 5; Mismatches 4; Indels
                                                                                         Fequence 33, Application US/10959310

Publication No. US20050287138A1

GENERAL INCRNATION:
TITLE OF INVENTION: CCR4 specific antibody composition
FILE REFERENCE: 249-363

CURRENT APPLICATION NUMBER: US/10/959,310

CURRENT FILING DATE: 2004-10-07

PRIOR FILING DATE: 2003-10-08

PRIOR PILING DATE: 2003-10-08

PRIOR PILING DATE: 2004-05-21

NUMBER OF SEQ ID NOS: 46

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 33

LENGTH: 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VS-10-959-310-26

Sequence 26, Application US/10959310

Publication No. US2000287138A1

GENERAL INFORMATION:
TILE OF INVENTION:
TILE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/959,310

CURRENT APPLICATION NUMBER: US/10/959,310

CURRENT PILING DATE: 2004-10-07

PRIOR APPLICATION NUMBER: US 60/572,784

PRIOR APPLICATION NUMBER: US 60/572,784

PRIOR APPLICATION NUMBER: 2004-05-21

NUMBER OF SEQ ID NOS: 46

SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) OTHER INFORMATION: Synthetic peptide US-10-959-310-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
91.8%;
Best Local Similarity 91.1%;
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-959-310-26
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LENGTH: 112
TYPE: PRT
                                                                                  US-10-959-310-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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Length 112; 4; Indels 9

Gaps

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Query Match
Best Local S
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j Sequence 54, Application US/11012353

j Publication No. US20050249730A1

j GENERAL INFORMATION:

APPLICANT: GOETSCH, LILIANE

j APPLICANT: CORVAIA, NATHALIE

APPLICANT: CORVAIA, NATHALIE

APPLICANT: DUFLOS, ALAIN

i TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

FILE REFERENCE: 01753-198

CURRENT PILLON UNMER: US/11/012,353

CURRENT PILLON DATE: 2004-12-16

PRIOR PLILON DATE: 2003-07-11

PRIOR PLILNG DATE: 2003-07-11

PRIOR APPLICATION NUMBER: FR 020553

PRIOR FILING DATE: 2003-07-20

PRIOR PLILNG DATE: 2003-07-20

PRIOR PLILNG DATE: 2003-07-20

PRIOR PLILNG DATE: 2003-07-20

PRIOR PLILNG DATE: 2002-01-8

PRIOR PLILNG DATE: 2002-01-8

PRIOR PLILNG DATE: 2002-01-8

PRIOR PLILNG DATE: 2002-01-18

PRIOR APPLICATION NUMBER: FR 020653

PRIOR PLILNG DATE: 2002-01-18

PRIOR APPLICATION NUMBER: FR 020654

PRIOR APPLICATION NUMBER: FR 020654

PRIOR APPLICATION NUMBER: FR 020654

PRIOR PLILNG DATE: 2002-01-18

NUMBER OF SEQ ID NOS: 162

SOFTWARE: PatentIn Ver. 3.3

SROT IN NO. 64
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Publication No. US20050249730A1

GENERAL INPORMATION:

APPLICANT: GOEYGCH, LILIANE

APPLICANT: CORVAIA, NATHALIE

APPLICANT: CORVAIA, NATHALIE

APPLICANT: HAEUW, JEAN-FRANCOIS

APPLICANT: LEGER, OLIVIER

APPLICANT: BECK, ALAIN

TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

FILE REFERENCE: 017733-198

CURRENT APPLICATION NUMBER: US/11/012,353

CURRENT PILING DATE: 2004-12-16

PRIOR PPLICATION NUMBER: FR 0308538

PRIOR PLING DATE: 2003-07-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCPGGSLLPWTFGGGTKVEIK 112
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Best Local Similarity 90.2<sup>3</sup>
Matches 101; Conservative
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CORGANISM: Mus musculus
US-11-012-353-54
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Sequence 56, Application US/11012353
; Sequence 56, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
    APPLICANT: CORVAIA, NATHALIE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: DUFLOS, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; FILE REFERENCE: 017773-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT PILING DATE: 2003-12-16
; PRIOR FILING DATE: 2003-07-11
; PRIOR FILING DATE: 2003-07-11
; PRIOR FILING DATE: 2003-07-07-11
; PRIOR FILING DATE: 2002-05-07
; PRIOR FILING DATE: 2002-05-07
; PRIOR FILING DATE: 2002-05-07
; PRIOR FILING DATE: 2002-01-08
; PRIOR FILING DATE: 2002-01-18
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PRIOR APPLICATION NUMBER: PCT/FR03/00178
PRIOR FILING DATE: 2003-01-20
PRIOR APPLICATION NUMBER: FR 0205753
PRIOR FILING DATE: 2002-05-07
PRIOR PILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARE: PALENTIN VOY: 3.3
LENGTH: 122
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SEQ ID NO 56
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; ORGANISM: Mus musculus
US-11-012-353-56
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Best Local Similarity
Matches 99; Conserv
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us-10-735-916a-61.rapbn

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TYPE: PRT
OKGANISM: Mus musculus
US-11-012-353-55
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| Publication No. US20550287148A1
| GENERAL INFORMATION:
| APPLICANT: Chatterjee, Malaya
| APPLICANT: Chatterjee, Sunil K.
| TITLE OF INVENTION: TREATMENT OF MELANOMA AND USE FOR THE
| TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
| TORRESPONDENCE 66
| CORRESPONDENCE ADDRESS:
| ADDRESSE: ADDRESSE:
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61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCPQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCPQGSHVPWTFGGGTKLEIK 131
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ZIP: 94304-1018

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentl Release #1.0, Version #1.30
SOFTWARE: 23-Mar-2005
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/089,266
FILING DATE: 23-Mar-2005
FILING DATE: 27-Mar-2005
FILING DATE: 1999-04-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 88.1%; Score 524; DB 7; Local Similarity 87.5%; Pred. No. 9e-35; nes 98; Conservative 9; Mismatches
                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Lin, Rong-Hwa
APPLICANT: Chang, Chung Nan
APPLICANT: Chen, Pei-Jiun
TITLE OF INVENTION: ANTIBODIES
FILE REPERENCE: 13062-011001
CURRENT APPLICATION NUMBER: US/11/125,837
CURRENT FILING DATE: 2008-05-10
PRIOR FILING DATE: 2004-05-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 100
SOFTWARR: FastSEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 131
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Mus musculus
US-11-125-837-23
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Best Local S:
Matches 98
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US-11-ULZ-13-15

Sequence 55, Application US/11012353

Publication No. US20050249730A1

GENERAL INFORMATION:

APPLICANT: GOETSCH, LILIANE

APPLICANT: CORVAIA, NATHALIE

APPLICANT: HAEUW, JEAN-FRANCOIS

APPLICANT: HAEUW, JEAN-FRANCOIS

APPLICANT: LEGER, OLIVIER

APPLICANT: LEGER, OLIVIER

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: NOVERED ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: NOVERED ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: NOVERED: 101753-199

CURRENT PILING DATE: 2004-12-16

PRIOR FILING DATE: 2003-12-16

PRIOR FILING DATE: 2003-07-11

PRIOR FILING DATE: 2002-05-07

PRIOR FILING DATE: 2002-01-18

PRIOR PILING DATE: 2002-01-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 263
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Pred. No. 2.3e-34;
APPLICATION NUMBER: US 08/372,676
FILING DATE: 1995-01-17
APPLICATION NUMBER: US 08/591,196
FILING DATE: 1996-01-16
ATTORNEY/AGENT INFORMATION:
NAME: Catherine M. Polizzi
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKEY NUMBER: 304142000202
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1813-5600
TELEFRANE: (415) 494-0792
TELERA: 706141
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acide
TYPE: amino acide
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SOFTWARE: PatentIn Ver. 3.3
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Matches 98; Conservative
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US-11-012-353-57
Sequence 57, Application US/11012353
Publication No. US20050249730A1
GENERAL INFORMATION:
APPLICANT: GORTSCH, LILIANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: DEGENOR, LILIANE
APPLICANT: LEGEN, OLIVIER
APPLICANT: RECEPTORS ANTIBODIES AND USES THEREOF
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
TITLE OF INVENTION NUMBER: US/11/012,353
CURRENT PILING DATE: 2003-12-16
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
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DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
                                        0; Gaps
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Search completed: January 10, 2006, 21:36:23 Job time : 6.71144 secs

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RESULT 2
US-10-735-916A-63
; Sequence 63, Application US/10735916A
; Publication No. US20050084906A1
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Matches 112; Conservative
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US-10-735-916A-61
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27, Appl
                                                                                                                           January 10, 2006, 20:53:43; Search time 61.4328 Seconds (without alignments) 761.757 Million cell updates/sec
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(gn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

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US-10-258-728-27

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US-10-31-452-13
US-10-505-980-20
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### ALIGNMENTS

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DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
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Sequence 61, Application WO 1020050084906A1

GENERAL INFORMATION:
APPLICANT: GOETSCH, Liliane
APPLICANT: COCKPALP, Nathalie
APPLICANT: DUFLOS, Alain
APPLICANT: DUFLOS, Alain
APPLICANT: DUFLOS, Alain
APPLICANT: BECK, Alain
APPLICANT: BECK, Alain
APPLICANT: BECK, Alain
APPLICANT: BECK, Alain
APPLICANT: WOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-183
CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT PILING DATE: 2003-12-16
FRIOR FILING DATE: 2003-07-11
FRIOR PELICATION NUMBER: FR 02/00 653
FRIOR PILING DATE: 2002-01-18
FRIOR APPLICATION NUMBER: FR 02/00 654
FRIOR APPLICATION NUMBER: FR 02/00 654
FRIOR APPLICATION NUMBER: FR 02/00 654
FRIOR PELING DATE: 2002-01-18
FRIOR FILING DATE: 2002-01-18
FRIOR FILING DATE: 2002-01-18
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FRIOR FILING DATE: 2002-05-07
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100.0%; Pred. No. 1.7e-46;
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US-10-735-916A-67
                                                                                                              Best Local Similarity
Matches 111, Conserv
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                                                   APPLICANT: CORVAIS...
APPLICANT: CORVAIS...
APPLICANT: CORVAIA. Nathalie
APPLICANT: LEGER, Olivier
APPLICANT: LEGER, Olivier
APPLICANT: DUFLOS, Alain
APPLICANT: BECK, Alain
APPLICANT: HAEUW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-183
CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT FILING DATE: 2003-07-11
FRIOR APPLICATION NUMBER: PCT/FR 03/00 178
FRIOR PELING DATE: 2003-07-11
FRIOR PELING DATE: 2002-01-18
FRIOR PELING DATE: 2002-01-18
FRIOR APPLICATION NUMBER: FR 02/00 653
FRIOR PELING DATE: 2002-01-18
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APPLICANT: CORTSCH, Liliane
APPLICANT: CORVAIA, Nathalie
APPLICANT: LEGER, Olivier
APPLICANT: BUFLOS, Alain
APPLICANT: BECK, Alain
APPLICANT: HAEUW, Jean-Francois
TITLE OF INVERTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-183
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100.0%; Score 595; DB 5; Length 131;
Best Local Similarity 100.0%; Pred. No. 2e-46;
Matches 112; Conservative 0; Mismatches 0; Indels 0
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CURRENT PILING DATE: 2003-12-16
PRIOR PAPLICATION NUMBER: E 03/08 538
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-01-20
PRIOR PILING DATE: 2003-01-00
PRIOR APPLICATION NUMBER: FR 02/06 653
PRIOR APPLICATION NUMBER: FR 02/06 654
PRIOR APPLICATION NUMBER: FR 02/06 654
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR SEQ ID NOS: 156
NUMBER OF SEQ ID NOS: 156
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Sequence 65, Application US/10735916A

Publication No. US20050084906A1
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CRGANISM: Homo sapiens
US-10-735-916A-63
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ORGANISM: Homo sapiens
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20 DIVWTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 79
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                                                                   Gaps
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Publication No. US20050084906A1
GENERAL INFORMATION:
APPLICANT: COCVAIA, Nathalie
APPLICANT: LEGER, Olivier
APPLICANT: LEGER, Olivier
APPLICANT: BECK, Alain
APPLICANT: BECK, Alain
APPLICANT: HARGW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-183
CURRENT APPLICATION NUMBER: FR 03/08 538
FRIOR APPLICATION NUMBER: FR 03/08 538
FRIOR APPLICATION NUMBER: PCT/FR 03/09 178
FRIOR FILING DATE: 2003-01-20
FRIOR FILING DATE: 2003-01-10
FRIOR FILING DATE: 2002-01-10
FRIOR FILING DATE: 2002-01-10
FRIOR APPLICATION NUMBER: FR 02/00 653
FRIOR FILING DATE: 2002-01-10
FRIOR APPLICATION NUMBER: FR 02/05 54
FRIOR FILING DATE: 2002-01-10
FRIOR APPLICATION NUMBER: FR 02/05 753
FRIOR FILING DATE: 2002-01-10
FRIOR FILING DATE: 2002-01-10
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   Length 112;
                                                               Indels
Score 594; DB 5; Lo Pred. No. 2.1e-46; 1; Mismatches 0;
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APPLICANT: Wother, Russell; APPLICANT: Wu, Dayang; TITLE OF INVENTION: HYBRID ANTIBODIES; FILE REFERENCE: 1087-37; CURRENT APPLICATION NUMBER: US/10/308,817; CURRENT FILING DATE: 2002-12-03; NUMBER OF SEQ ID NOS: 195
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FEATURE:
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APPLICANT: Motoo YAMASAKI
APPLICANT: AALKA FURUYA
APPLICANT: AALKA TURUYA
APPLICANT: Kenya SHITARA
APPLICANT: Renya SHITARA
APPLICANT: Naoki SHIMADA
TITLE OF INVENTION: Anti-fiblroblast growth factor-8 monoclonal antibod
FILE REFERENCE: 249-310
CURRENT APPLICATION NUMBER: US/10/434,469
CURRENT FILING DATE: 2003-05-09
                                                                                                                                                                                            1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                                                                                                                                            0; Gaps
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                                                                                                                                                            3; Indels
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Pred. No. 1.4e-43;
4; Mismatches 3;
                                                                                                                        94.6%; Score 563; DB 4;
93.8%; Pred. No. 1.4e-43;
iive 4; Mismatches 3;
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TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 82 CIP (1087-37 CIP)
CURRENT APPLICATION NUMBER: US/10/453,698
CURRENT FILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 196
SOFTWARE: Patentin version 3.2
LENGTH: 112
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PRIOR FILING DATE: 1996-04-03
PRIOR APPLICATION NUMBER: US 08/832,236
PRIOR FILING DATE: 1997-04-03
PRIOR APPLICATION UNUBER: US 09/326,590
PRIOR FILING DATE: 1999-06-07
PRIOR APPLICATION NUMBER: US 09/876,040
                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 182, Application US/10453698
; Publication No. US20040038308A1
; GENERAL INFORMATION:
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Publication No. US20040091480A1
GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.1
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Best Local Similarity 93.8 Matches 105; Conservative
                                                                                                                        Query Match
Best Local Similarity 93.8
Matches 105; Conservative
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ORGANISM: human
                                                 ; TYPE: PRT
; ORGANISM: human
US-10-308-817-182
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US-10-453-698-182
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                   SEQ ID NO 182
                                    LENGTH:
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US-10-258-728-28

Sequence 28, Application US/10258728

Publication No. US20040091485A1

Hublication No. US20040091485A1

APPLICANT: Ellis, John Robert Maxwell

APPLICANT: Durrant, Linda Gillian

TITLE OF INVENTION: Humanised Antibodies to the Epidermal Growth Factor Receptor

FILE REFERENCE: 28438-101US01

CURRENT APPLICATION NUMBER: US/10/258,728

PRIOR PILING DATE: 2000-06-18

PRIOR APPLICATION NUMBER: GB 0011981.8

PRIOR PILING DATE: 2000-06-19

PRIOR PILING DATE: 2000-05-19

PRIOR PILING DATE: 2000-08-24

NUMBER OF SEQ ID NOS: 28

SOFTWARE: PatentIn version 3.1

SEQ ID NO 28

LENGTH: 112
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Sequence 17, Application World US/2040253234A1
Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, September 18, Sequence 17, September 18, September
                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: VL synthetic peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.6%; Score 563; DB 4; Length 112;
93.8%; Pred. No. 1.4e-43;
tive 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial Sequence
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 112
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Best Local Similarity 93.8%
Matches 105; Conservative
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Best Local Similarity
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US-10-434-469-19
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LENGTH: 112
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                                                                                                                                                                                                  Length 112;
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Best Local Similarity 93.8%; Pred. No. 1.4e-43;
Matches 105; Conservative 5; Mismatches 2; Indels
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Publication No. US20050175608A1
GENERAL INPORMATION:
APPLICANT: KYOWA HAKKO KOGYO CO., LTD
TITLE OF INVENTION: AGENT FOR TREATING ARTHRITIS
FILE REFERENCE: 1442
CURRENT APPLICATION NUMBER: US/10/500,207A
CURRENT FILING DATE: 2004-06-28
PRIOR FILING DATE: 2001-12-28
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Publication No. US20050175608A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: AGENT FOR TREATING ARTHRITIS
FILE REFERENCE: 1442
CURRENT APPLICATION NUMBER: US/10/500,207A
CURRENT FILING DATE: 2004-06-28
PRIOR APPLICATION NUMBER: JP2001-400677
PRIOR FILING DATE: 2001-12-28
NUMBER OF SEQ ID NOS: 51
SOFTWARE PATENTIN Version 3.1
SEQ ID NO 47
                                                                                                                                                                                                Query Match 94.6%; Score 563; DB 5; L. Best Local Similarity 93.8%; Pred. No. 1.4e-43; Matches 105; Conservative 5; Mismatches 2;
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SOFTWARE: Patentin version 3.1
SEQ ID NO 19
EMCTH: 112
                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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  SOFTWARE: Patentin Ver.
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                      SEQ ID NO 17
LENGTH: 112
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                                                                                                            FEATURE:
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APPLICANT: Ellis, John Robert Maxwell
APPLICANT: Ellis, John Robert Maxwell
APPLICANT: Durrant, Linda Gillian
TITLE OF INVENTION: Humanised Antibodies to the Epidermal Growth Factor Receptor
TITLE REPERENCE: 28438-101US01
CURRENT APPLICATION NUMBER: 05/10/258,728
CURRENT FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: GB 0011981.8
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                                                                                OTHER INFORMATION: LV.2-2, a designed amino acid sequence of VL of OTHER INFORMATION: an anti-FGF-8 CDR-grafted neutralizing antibody
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| Sequence 6, Application US/10388214A
| Publication No. US20040082762A1
| GENERAL INFORMATION:
| APPLICANT: Basi, Guriq
| APPLICANT: Saldanha, Jose
| TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE BETA
| TITLE OF INVENTION: AMYLOID PEPTIDE
| FILE REFERENCE: EIN-004
| CURRENT PELLING DATE: 2003-03-12
| PRIOR APPLICATION NUMBER: US 60/363,751
| PRIOR APPLICATION NUMBER: US 60/363,751
| WUMBER OF SEQ ID NOS: 38
| SOFTWARE: PRECES for Windows Version 4.0
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93.8%; Pred. No. 2.6e-43;
tive 5; Mismatches 2; Indels
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94.1%; Score 560; DB 4; L.
Best Local Similarity 94.6%; Pred. No. 3.1e-43;
Matches 106; Conservative 3; Mismatches 3;
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TYPE: PRT
ORGANISM: Artificial Sequence
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US-10-388-214A-6
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                                                                                                                         ; OTHER INFORMAT
US-10-500-207A-47
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US-10-258-728-27
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Sequence 26, Application No. US20040091485A1

GENERAL INFORMATION:

APPLICANT: Blis, John Robert Maxwell

APPLICANT: Blis, John Robert Maxwell

TITLE OF INVENTION: Humanised Antibodies to the Epidermal Growth Factor Receptor

FILE REFERENCE: 28438-101US01

CURRENT APPLICATION NUMBER: US/10/258,728

CURRENT APPLICATION NUMBER: GB 0011981.8

PRIOR FILING DATE: 2000-06-18

PRIOR FILING DATE: 2000-06-24

NUMBER OF SEQ ID NOS: 28

SEQ ID NOS: 28

LENGTH: 112
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APPLICANT: Akiko FURUYA
APPLICANT: Akira TNANKA
APPLICANT: Kenya SHITARA
APPLICANT: Kenya SHITARA
APPLICANT: NOOK'S SHIMADA
ITITE OF INVENTION: Anti-fiblroblast growth factor-8 monoclonal antibod
FILE REFERENCE: 249-310
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Pred. No. 3.2e-43;
3; Mismatches 5
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: GB 0020794.4
PRIOR FILING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.1
SEQ ID NO 27
LENGTH: 112
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Publication No. US20040091480A1
GENERAL INFORMATION:
APPLICANT: Nobuo HANAI
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Best Local Similarity 92.9%;
Matches 104; Conservative
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Best Local Similarity 92.9
Matches 104; Conservative
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; ORGANISM: Mus musculus
US-10-258-728-27
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OTHER INFORMATION: Description of Artificial Sequence: LV.3-1 of VL of KM8036
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                   CURRENT FILING DATE: 2003-05-09
PRIOR APPLICATION NUMBER: JP 08-081754
PRIOR FILING DATE: 1996-04-03
PRIOR FILING DATE: 1997-04-03
PRIOR RELING DATE: 1997-04-03
PRIOR APPLICATION NUMBER: US 09/326,590
PRIOR APPLICATION NUMBER: US 09/326,690
PRIOR FILING DATE: 1999-06-07
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN VET. 2.1
CURRENT APPLICATION NUMBER: US/10/434,469
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ORGANISM: Artificial Sequence
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                                                                           January 10, 2006, 20:34:27; Search time 21.8706 Seconds (without alignments) 423.384 Million cell updates/sec
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(cgn2_6/ptodata/1/iaa/6_COMB.pep:*
(cgn2_6/ptodata/1/iaa/H_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PGTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd.
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US-08-331-397B-50
US-08-31-397B-50
US-09-227-693-50
US-08-053-171-15
US-08-015-190A-14
US-08-129-930B-95
US-08-134-346A-95
US-08-134-346A-95
US-08-482-882-66
US-08-482-882-66
US-08-483-389-66
US-08-483-389-66
US-08-473-503-66
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US-08-473-69
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S-09-192-838B-2
S-09-324-191-2
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-08-077-252B-3
                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-331-397B-48
US-08-759-804A-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -08-752-844-66
                                                                                                                                                                                                                               572060 segs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                   - protein search, using sw model
                                                                                                                                                                                                    Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                     seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
Match Length
            Copyright
                                                                                                                                                                                       BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
                                                                                                                                                Perfect score:
                                                   OM protein
                                                                                                                                                                                                                                                                                     Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                    Database :
                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                Searched:
                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Result
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Appl	29,	Sequence	US-08-207-861-29	0	112	87.1	518	45
App	61	Sequence	US-08-207-861-19	0	112	87.1	518	44
Appl	29,	Sequence	US-08-859-649-29	7	112	87.1	518	43
App]	13	Seguence	US-08-859-649-19	ч	112	87.1	518	42
App	34,	Sequence	US-08-759-804A-34	ч	248	87.4	520	41
App	34,	Sequence	US-08-331-397B-34	П	248	87.4	520	40
Appl	34,	Sequence	US-08-331-398A-34	н	248	87.4	520	39
Appl	34,	Sequence	US-09-227-693-34	N	247	87.4	520	38
Appli	7	Sequence	US-09-293-533-2	N	149	87.4	520	37
Appli	7	Sequence	US-08-591-196-2	н	149	87.4	520	36
Appli	ς,	Sequence	US-08-752-844-2	Н	149	87.4	520	35
Appl	99	Sequence	US-08-759-804A-66	ч	125	87.4	520	34
Appl	67,	Sequence	US-08-331-397B-67	-	125	87.4	520	33
Appl	67,	Sequence	US-08-331-398A-67	Н	125	87.4	520	32
Appli	۳,	Sequence	PCT-US94-06687-3	4	112	87.4	520	31
Appli	m,	Sequence	US-09-657-274-3	7	112	87.4	520	30
Appl	48,	Sequence	US-09-227-693-48	N	112	87.4	520	29
3, Appli	3,	Sequence	US-09-002-753A-3	7	112	87.4	520	28

# ALIGNMENTS

```
Sequence 50, Application US/08331398A

Sequence 50, Application US/08331398A

Patent No. 560039

GENERAL INFORMATION: Ira

APPLICANT: Pastan, Ira

APPLICANT: Pastan, Lee

APPLICANT: Pati, Lee

TITLE 0F INVENTION: Single Chain B3 Antibody Fusion Proteins

TITLE 0F INVENTION: and Their Uses (as amended)

NUMBER OF SEQUENCES: 66

CORRESPONDESSEB: Townsend and Townsend and Crew

STREET: One Market Plaza, Steuart Street Plaza

STRATS: California

COUNTRY: USA Prancisco

STRATS: California

COUNTRY: USA Prancisco

STRATS: Pation Market Plaza, Steuart Street Plaza

STRATS: California

COUNTRY: USA Prancisco

STRATS: Pation Market Plaza, Steuart Street Plaza

STRATS: California

COUNTRY: USA Prancisco

STRATS: Pation Market Plaza, Steuart Street Plaza

STRATS: California

COUNTRY: USA Prancisco

STRATS: Pation Market Plaza, Steuart Street Plaza

STRATS: 28-07T-1994

FILING DATE: 28-07T-1994

FILING DATE: 28-07T-1994

FILING DATE: 29-05T-1990

ATTORNEY/AREN INFORMATION:

REGISTRATION NUMBER: US 07/767,331

PRIOR APPLICATION NUMBER: US 07/767,331

PRIOR APPLICATION NUMBER: US 07/767,331

PRIOR APPLICATION NUMBER: US 07/767,331

FILING DATE: 12-07T-1990

ATTORNEY/AREN INFORMATION:

NAME: HUITEY: Tom

REGISTRATION NUMBER: US 07/767,331

FILING DATE: 12-07T-1990

ATTORNEY ARENT INFORMATION:

NAME: HUITEY: Tom

REGISTRATION TOWERS: 13-560

TELEPAN: (415) 543-560

TELEPAN: (415) 543-560

TELEPAN: (115) 543-560

TELEPAN: (115) 543-560

TELEPAN: (115) 543-560

TELEPAN: (115) 543-560

TELEPAN: USE OF DECENTION NUMBERS: US 07/767

SEQUENCE CHARATERISTICS:

LENGTH: 112 amino acid

TELEPAN: USE DECENTION NUMBERS:

SEQUENCE THERES:

SEQUENCE TH
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Query Match

Best Local Similarity 94.6%;
Matches 106; Conservative 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
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                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Pastan, Ira
APPLICANT: Benhar, Itai
TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEB: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Plaza
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIXKVSNRL 60
                                                                                                                                                                                                                                                                           DVLMTQSPLSLPVTPGEPASISCRSSQIIVHSNGNTYLEWYLQKPGQSPQLLIYKVSNRF 60
                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                        Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Humanized B3 Variable Light
chain (V-L) (HumB3V-L)"
                       LOCATION: 1..112
OTHER INFORMATION: /note= "Humanized B3 Variable Light
OTHER INFORWATION: Chain (V-L) (HumB3V-L)"
                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/331,397B
FILING DATE: 28-CT-1994
CLASSIFICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION NUMBER: US 07/767,331
FILING DATE: 12-CT-1990
ATTORNEY/AGENT INFORMATION:
NAME: HUNTEY, TOM
                                                                                                                                       Score 560; DB 1;
Pred. No. 1.8e-47;
3; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REPERENCE/DOCKET NUMBER: 015280-126120US
TELEPHONE: (415) 543-5600
TELEPHONE: (415) 543-5601
TELEPHONE: (415) 543-5601
INPORMATION FOR SEQ ID NO: 50: SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-331-397B-50
; Sequence 50, Application US/08331397B
; Patent No. 5981726
; GENERAL INFORMATION:
                                                                                                                                       Query Match
Best Local Similarity 94.6%;
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
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); OTHER INFORMATION:

US-08-331-397B-50
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US-08-331-398A-50
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1 DVLMTQSPLSLPVTPGEPASISCRSSQIIVHSNGNTYLEWYLQKPGQSPQLLIYKVSNRF 60
                                                                                                                                                                                       1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                     61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                         61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCPQGSHVPFTFGQGTKVEIK 112
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                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
US-08-759-804A-50
is Sequence 50, Application US/08759804A
is Patent No. 5990296
is GENERAL INFORMATION:
APPLICANT: Patent, Ira
APPLICANT: Patent, Ira
APPLICANT: Patent, David J.
APPLICANT: Patent David J.
APPLICANT: David J.
APPLICANT: Patent David J.
APPLICANT: Patent David J.
APPLICANT: Patent David J.
APPLICANT: Patent David J.
APPLICANT: David J.
APPLICANT: Patent J.
APPLICANT: Patent J.
APPLICANT: David J.
APPLICANT: Patent J.
APPLIC
Score 560; DB 1; Length 112;
Pred. No. 1.8e-47;
3; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 05/096
CLASSIFICATION NUMBER: 08/096
CLASSIFICATION NUMBER: 08/097
FILING DATE: 08/031,398
FILING DATE: 28/0CT-1994
PRIOR APPLICATION NUMBER: 08/031,398
FILING DATE: 28/0CT-1994
PRIOR APPLICATION NUMBER: 08/07/67,331
FILING DATE: 38/0CT-1991
PRIOR APPLICATION NUMBER: 08/07/67,331
FILING DATE: 32-0CT-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 015280-126140US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 01521
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 1.112
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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PEATURE:
NAMEZ/KEY: REGION
LOCATION: 24.39
OTHER INFORMATION:
OTHER INFORMATION:
PRATURE:
NAMEZ/KEY: REGION
LOCATION: 55.61
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Region
LOCATION: 94..102
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1.112
OTHER INFORMATION:
Patent No. 5562903
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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                                                                                             1 DVVWTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gape
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 50, Application US/09227693
Sequence 50, Application US/09227693
Patent No. 6287562
GENERAL INFORMATION:
APPLICANT: PRAIAN, Irai
APPLICANT: PADLAN, Eduardo A.
APPLICANT: JUNG, Sun-Hee
                                                                                                                                                                                                                                                       61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCPQGSHVPFTFGQGTKVEIK 112
                                                                                                                                                                                                                    61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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94.1%; Score 560; DB 2; Length 112;
Best Local Similarity 94.6%; Pred. No. 1.8e-47;
Matches 106; Conservative 3; Mismatches 3; Indels
                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 1..112
OTHER INFORMATION: /note= "Humanized B3 VL region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza CITY: San Prancisco CITY: California COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94105-1493

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/227,693
94.6%; Pred. No. 1.8e-47; tive 3; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRILING DATE:
PRICOR ADDICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15280-126-1-3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/331,396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 112 amino acida
TYPE: amino acid
STRANDEDNESS: single
Best Local Similarity 94.6
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-227-693-50
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Query Match
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                                                                                                                                                                                                                                                                                                                               1 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLEWYLQKPGQSPQLLISKVSNRF 60
                                                                                                                                                                                                                                                                                    1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                                                                                                                                                                                                                             Gaps
                                                                                    /note= "Residue in the framework that is replaced with mouse amino acid in the humanized antibody."
                                                                                                                                                                                                                                                                                                                                                                           61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVBIK 112
                                                                                                                                                                                                                                                                                                                                                                                                  61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPFTFGQGTKLEIK 112
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Sequence 14, Application US/08815190A

Batent No. 6046310

GENERAL INFORMATION:
APPLICANT: Queen, Cary L.
APPLICANT: Queen, Cary L.
APPLICANT: Queen, William P.
APPLICANT: General Maximiliano
ITILE OF INVENTION: Uses Ligand Fusion Proteins and Their
ITILE OF INVENTION: Uses
NUMBER OF SEQUENCES: 17
CORRESPONDENCES: 17
CORRESPONDENCE ADDRESSE: 190
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Prancisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                  Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "mature light chain variable region of humanized ABL 364 antibody"
                                                                                                                                                                                                                                      3; Indels
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MEDIUM TYPE: 1834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,190A
FILING DATE: 11-MAR-1997
CLASSIPICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/614,584
FILING DATE: 13-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 011823-006710US
TELEFENNE (415) 576-0200
TELEFENNE: (415) 576-0200
TELEFENNE: (415) 576-0300
TELEFENCE CHARACTERICING:
SEQUENCE CHARACTERICING:
SEQUENCE CHARACTERICING:
COMPUTATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERICING:
                                                                                                                                                                                             Score 556; DB 1;
Pred. No. 4.4e-47;
4; Mismatches 3;
OTHER INFORMATION: antibody."
                                                                                                                                                                                                  93.4%;
93.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS:
                                         Modified-site
                                                                                                                                                                                                                                           Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION:
; OTHER INFORMATION:
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US-08-815-190A-14
                                                                                  OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                               Query Match
Best Local Similarity
                      FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-815-190A-14
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                                                                                                                 20 DVLMTQTPLSLPVTPGEPASISCRSSQSIVHSNGNTYLEWYLQKPGQSPQLLIXKVSIRF 79
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                                                 Gaps
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                                                                                                                                                                            61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                     61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCPQGSHVPFTFGQGTKLEIK 112
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Fatent No. 5804187
GENERAL INFORMATION:
APPLICANT: do Couto Dr., Pernando J.R.
APPLICANT: Peterson Dr., Roberto L.
APPLICANT: Peterson Dr., Borry A.
APPLICANT: Peterson Dr., Eduardo A.
TITLE OF INVENTION: Analogue Peptides With Broad
TITLE OF INVENTION: Carcinoma Specificity, and Kit and
TITLE OF INVENTION: Therapeutic Methods
MUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: V. AMZEL & ASSOC.
Score 556; DB 2; Length 112;
Pred. No. 4.4e-47;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 2055 No. 5804187th Broadway, Suite 201 CITY: Walnut Creek STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO comparible
OPERATUS SYETEM: PC-DOS/MS-DOS 5.0
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: September 30, 1993
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 544; DB 1;
Pred. No. 7.7e-46;
6; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Amzel Ph.D., Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: CRFCC-008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 521-1333
TELEFAX: (510) 521-3541
    93.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: n.a. INFORMATION FOR SEQ ID NO: 95:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 131 amino acids
                                               Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide US-08-129-930B-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 102; Conserve
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                           Similarity
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                             Best Local
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.4%;
91.1%;
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Best Local Similarity 91.1'
Matches 102; Conservative
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MEDIUM TYPE: Floppy
CITY: Los Angeles
STATE: California
COUNTRY: USA
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                                                                                         APPLICANT: do Couto, F.J.R.
APPLICANT: Ceriani, R.L.C.
APPLICANT: Petersen, J.A.
TITLE OF INVENTION: HYBRIDOMA AND ANTI-KC-4 HUMANIZED
TITLE OF INVENTION: MONOCLONAL ANTIBODY AND DNA AND RNA ENCODING IT, KIT AND
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 SGVPDRFSGSGSGTDFTLKISRVEAEDVGIYYCFQGSHVPYTFGGGTKLEIK 131
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Patent No. 6315997
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ceriani Dr., Fernando J.R.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Peterson Dr., Zerry A.
TITLE OF INVENTION: Analogue Peptides With Broad
TITLE OF INVENTION: Analogue Peptides With and
TITLE OF INVENTION: Therapeutic Methods
ITTLE OF INVENTION: Therapeutic Methods
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSE: PETELY, Schroeder & Poplawski
STREET: 444 South Flower St., 19th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: US

ZIP: 10022-7499

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-3.50 inch, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE STATES.

SOFTWARE STATES.

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/134,346A

FILING DATE: 08-OCT-1993

CLASSIFATION:

ATTORNEY/AGENT INFORMATION:

NAME: OFFICIAL STATES.

REFERENCE/DOCKET NUMBER: 31,889

REFERENCE/DOCKET NUMBER: CLT 149,608

TELEPHONE: 212-826-5509

INFORMATION FOR SEQ ID NO: 50:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:
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91.4%; Score 544; DB 2;
Best Local Similarity 91.1%; Pred. No. 7.7e-46;
Matches 102; Conservative 6; Mismatches 4;
                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSER: Oetrager, Chong & Flaherty
STREET: 300 Park Avenue
CITY: New York
                 Sequence 50, Application US/08134346A Patent No. 6281335 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 131 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS
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    US-08-134-346A-50
                                                                                                                                                                                                                                                                                                                                                             STATE:
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1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
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; Sequence 66, Application US/08482882
; Patent No. 5773218
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
; TITLE OF INVENTION: ICAM-Related Materials and Methods
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: Giolo Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 544; DB 2; Length 131;
Pred. No. 7.7e-46;
6; Mismatches 4; Indels
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORPTARE: BACENTIN Release #1.0, Version #1.25
SOCTAMEN: PACENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,288A
FILING DATE: No. 6315997ember 21, 1997
CLASSIFICATION NUMBER: 08/129,930
FILING DATE: September 30, 1993
PRIOR APPLICATION NUMBER: 07/977,696
FILING DATE: No. 6315997ember 16, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel Ph.D.
REGISTRATION NUMBER: 30, 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,882
FILING DATE: 07-UN-1995
CLASSIPICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: P6639938
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 DIVWTQSPLSLPVTPGEPASISCRSSQSLVHSNGDTYLHWYLQKPGQSPQLLIYKVSNRF 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTHVPYTFGQGTKVEIK 116
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Patent No. 5811517

GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-RELATED PROTEIN
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: Olited States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.3%; Score 543; DB 1; Length 116; 91.1%; Pred. No. 8.5e-46; tive 5; Mismatches 5; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/286,754
FILING DATE:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/899,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5773218and, Greta E.
REGISCHANICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRONE: (312) 474-630
TELEFRAX: (312) 474-630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/483,389
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
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Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-08-482-865
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US-08-483-389-66
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPTTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,503
PILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/286,754
FILING DATE: 05-AUG-1994
APPLICATION NUMBER: US 08/102,852
PILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO .5837822and, Greta E. REGISTRATION NUMBER: 35,302
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (312) 474-6300
TELERAX: (312) 474-6300
TELERAX: 25-3856
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-487-113D-66
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1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
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Patent No. 5880268
GENERAL INFORMATION:
APPLICANT: Vacaux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSEE:
ADDRESSEE: ADDRESSEE:
STREET: 6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CALF: 50000

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,932
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/286,754
FILING DATE: 05-AUG-1994
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION 
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-UN-1992
PRICR APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRICR APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5869265and, Greta E.
REGISTATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32178
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-6448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 102; Conservative
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MOLECULE TYPE: protein
US-08-473-503-66
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
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US-08-483-932-66
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Search completed: January 10, 2006, 20:58:03 Job time : 22.8706 secs
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i Sequence 66, Application US/08720420A

i Patent No. 5989843

general INFORMATION:

APPLICANT: Gallatin, W. Michael

APPLICANT: Wazeux, Rosemay

ITILE OF INVENTION:

CORRESPONDENCES: 120

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 91.3%; Score 543; DB 1; Length 116; Best Local Similarity 91.1%; Pred. No. 8.5e-46; Matches 102; Conservative 5; Mismatches 5; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,420A
APPLICATION NUMBER: US UNIGERIA PRICING DATE: 05-UNN-1992
PRICING DATE: 05-UNN-1992
PRICINATION NUMBER: US 07/889,724
PILING DATE: 26-MAY-1992
PRICINA APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5880268and, Greta E. REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32178
TELECOMMUNICATION INFORMATION:
TELECHONE: (312) 474-6300
TELECHONE: 132) 474-6300
TELECHONE: 25-386
INFORMATION FOR SEQ ID NO: 66: SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,113
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/286,754
FILING DATE: 05-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein US-08-483-932-66
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1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 91.3%; Score 543; DB 1; Length 116; Best Local Similarity 91.1%; Pred. No. 8.5e-46; Matches 102; Conservative 5; Mismatches 5; Indels
PRICING DATE: 26-000.

PRIOR APPLICATION DATA: 378-1016.

APPLICATION NUMBER: US 07/894,061

FILING DATE: 05-00N-1992

PRIOR APPLICATION DATA: 36-1016.

PRIOR APPLICATION NUMBER: US 07/827,689

PRIOR APPLICATION NUMBER: US 07/827,689

PILING DATE: 27-0AN-1992

ATTORNEY/AGENT INFORMATION: NAME: Williams, Joseph A., Jr. REGISTRATION NUMBER: 38,659

REFERENCE/ODCKET NUMBER: 33.282

TELECOMMUNICATION: NUMBER: 33.282

TELECOMMUNICATION INFORMATION: TELECHNOR: (312) 474-6300

TELEFRAX: (312) 474-6300

TELEFRAX: 35-3856

INFORMATION FOR SEQ ID NO: 66: SEQUENCE CHARACTERISTICS: LENGTH: 116 amino acids

TYPE: amino acids

TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-720-420A-66
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

January 10, 2006, 20:28:02; Search time 13.5124 Seconds (without alignments) 797.508 Million cell updates/sec

1 DVVMTQSPLSLPVTPGEPAS......CPQGSHVPWTFGQGTKVEIK 112 US-10-735-916A-61 Perfect score: Sequence:

283416 segs, 96216763 residues Gapop 10.0 , Gapext 0.5 Searched:

**BLOSUM62** 

Scoring table:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	chain		chain -	chain	chain	kappa chain V r	_	chain	chain	chain	chain		chain	chain		chain	chain	chain		chain		chain	chain	chain	chain	chain		chai	kappa chain V r
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SUMMARIES	Ц	6		8	7	3																							2	ហ
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	DB	~	~	7	7	7																					~			N
	* Query Match Length DB	131	113	219	112	21		112	112	136	114	118	131	112	112						112	131	132	133			131		135	112
	Query Match	88.1	_	86.9	ø	w	Ψ	86.2	86.2	86.2	85.7	85.5	85.5	85.2	84.9	84.9		84.4	84.4	84.2	84.0	84.0	84.0	84.0	84.0	•	83.9	•	83.9	83.7
	Score	524	523	517	514	514	513	513	513	513	510	509	509	507	505	505	503	502	502	501	200	200	200	200	200	499	499	499	499	498
	Result No.	-	7	e	4	ß	φ	7	8	σ,	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

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K2HUGM PI.0257	A49715	853750	B41940	832189	JL0029	S40339	S22902	A24452	D27887	D29380	S23230	B27887	S40356	G34903
ч	1 (1	7	N	N	~	7	7	Н	N	7	N	~	7	N
117	112	112	113	112	225	126	142	133	112	131	133	112	125	131
83.7	83.5	83.2	83.2	83.0	83.0	82.9	82.9	82.7	82.5	82.5	82.5	82.4	82.4	82.4
498	497	495	495	494	494	493.5	493	492	491	491	491	490	490	490
30	3 7	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

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RESULT 1

19 149ht chain precursor V-D-J region (6-19) - mouse

19 159ht chain precursor V-D-J region (6-19) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 21-Jan-2000

C;Accession: B39276 # Sequence\_revision 18-Oct-1991 #text\_change 21-Jan-2000

C;Accession: B39276 # Sequence\_revision 18-Oct-1991 #text\_change 21-Jan-2000

R;Reininger, L: Berney, T.; Shibata, T.; Spertini, F.; Merino, R.; Izui, S.

Proc. Natl. Acad. Sci. U.S.A. 87, 10038-10042, 1990

A;Title: Cryoglobulinemia induced by a murine 1gG3 rheumatoid factor: skin vasculitis an A;Accession: B39276; MUD:91088540; PMID:2263605

A;Status: preliminary A;Molecule type: mRVA A;Residues: 1-131 <PRE: A A;Cross-references: UNIPARC:UP10000115153; GB:M55313; NID:g198095; PIDN:AAA63385.1; PID C;Superfamily: immunoglobulin V region; immunoglobulin homology

C; Keywords: immunoglobulin F; 35-114/Domain: immunoglobulin homology < IMM>

ö Gaps .. 0 Query Match 88.1%; Score 524; DB 2; Length 131; Best Local Similarity 87.5%; Pred. No. 1.6e-42; Matches 98; Conservative 9; Mismatches 5; Indels

1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60 20 DVLATQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIXKVSNRF 79 셤 ઠ

61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCPQGSHVPWTFGQGTKVEIK 112 ઠે

80 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPYTFGSGTKLEIK 131 셤

## RESULT 2

arti-DNA autoantibody BV17-31, kappa chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000
C;Accession: PLO203
R;Smith, R.G.; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1990
A;Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from 1 A;Reference number: PLO198; MUID:90309768; PMID:2114528
A;Reference region primary structures of monoclonal anti-DNA autoantibodies from 1 A;Residues: 1-113 <SMIA
A;Residues: 1-113 <SMIA
A;Cross-references: UNIPARC:UPI0000113786; GB:X53643; NID:g50196; PIDN:CAA37694.1; PID::C;Superfamily: immunoglobulin homology <IVM'>F;16-95/Domain: immunoglobulin homology <IVM'>F;16-95/Domain: immunoglobulin homology <IVM'>F;16-95/Domain: immunoglobulin homology <IVM'>F;16-95/Domain: complementarity-determining 3
F;34-39/Region: complementarity-determining 3
F;34-102/Region: complementarity-determining 3
F;101-113/Region: D region

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A;Molecule type: mRNA
Mresiduce: 1-219 KKMA.
A;Cross-references: UNIPARC:UPI00001157E4; GB:U29147; NID:g1594225; PIDN:AAC52821.1; PID.
C;Comment: This protein is specific for human plasma apolipoprotein A-I of high-density
C;Superfamily: immunoglobulin V region; immunoglobulin homology
E;1-112/Domain: V region #status predicted <VRG>
P;113-219/Domain: C region #status predicted <CRG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: 826335
R;Stark, S.B.; Caton, A.J.
B.E. Med. 174, 613-644, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein e. A;Reference number: $26309; MUID:91341421; PMID:1908510
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                                                                                                                                                                                                                                                                      C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000
C;Accession: PC4203
R;Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.
Gene 173, 257-259, 1996
A;Fitle: Cloning and characterization of cDNAs coding for heavy and light chains A;Reference number: PC4202; MUID:97082978; PMID:8964510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
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61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                    61 SGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWOGSHVPYTFGGGTKLEIK 112
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Pred. No. 1.4e-41;
9; Mismatches 5; Indels
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                                                                                                                                                                                                                                         Ig kappa chain (monoclonal antibody MabA34) - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Indels
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Ig light chain V region anti-F(ab')2 - human (fragment)
C:Species Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 514; DB 2;
Pred. No. 2.5e-41;
9; Mismatches 6;
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Best Local Similarity 87.3%;
Matches 96; Conservative
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A;Residues: 1-110 <STA>
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Best Local (
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A31807
Iq kappa chain V region (PAC1) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 20-Jul-1989 #sequence_revision 20-Jul-1989 #text_change 09-Jul-2004
C;Accession: A31807
R;Taub, R.; Gould, R.J.; Garsky, V.M.; Ciccarone, T.M.; Hoxie, J.; Friedman, P.A.; Shatt J. Biol. Chem. 264, 259-265, 1989
A;Title: A monoclonal antibody against the platelet fibrinogen receptor contains a seque A;Reference number: A31807
A;Accession: A31807
A;Accession: A31807
A;Accession: A31807
A;Residues: 1-112 <TAU>
A;Residues: 1-112 <TAU>
C;Auperfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology <IMM>
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C; Species: Mus muscules (house mouse)
C; Species: Mus muscules (house mouse)
C; Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C; Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C; Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
R; year Engelon: F; Schouten, A.; Molthoff, J.W.; Roosien, J.; Dirkse, W.G.; Schots, A.; Pabmitted to the EMBL Data Library, August 1994
A; Reserrence number: S52028
A; Accession: S52028
A; Residues: 1-219 < VAN>
A; Residues: 1-210 < VAN>
A; Re
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                                    Length 113;
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Pred. No. 1.3e-41;
6; Mismatches 7; Indels
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86.4%; Score 514; DB 2; Length 11
1 Similarity 85.7%; Pred. No. 1.2e-41;
96; Conservative 11; Mismatches 5; Indels
                                                                                                      Indels
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                             ; DB 2;
1.7e-42;
                             ch 87.9%; Score 523; DB 1 Similarity 87.5%; Pred. No. 1.7e 98; Conservative 9; Mismatches
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Best Local Similarity 88.4%;
Matches 99; Conservative
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Best Local Similarity
Matches 96; Conserv
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A;Cross-references: UNIPROT:QBNEKO; UNIPARC:UPI0000176CA8; EMBL:X72467 C;Superfamily: immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;36-115/Domain: immunoglobulin homology <IMM>
                                                                                                                                                   Query Match
Best Local Similarity 86.6
Matches 97; Conservative
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A; Residues: 1-118 < SHE>
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   C; Date: 13-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 21-Jan-2000
C; Accession: S58207
R; Melschof, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebel, S.; Breitling, submitted to the EMBL Data Library. July 1995
A; Description: Characterization of heavy and light chain immunoglobulin variable region A; Accession: S58206
A; Accession: S58207
A; Accession: Description: Characterization of heavy and light chain immunoglobulin variable region A; Accession: BS8207
A; Accession: S58207
A; A; Accession: S58207
A; Cross-references: UNIPARC: UPI0000116253; EMBL: X89056; NID: 9929642; PIDN: CAA61443.1; PICCES-references: UNIPARC: UPI0000116253; EMBL: X89056; NID: 9929642; PIDN: CAA61443.1; PICCES-references: Immunoglobulin V region; immunoglobulin homology
C; Keywords: immunoglobulin homology <IMM>
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C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 31-Dec-2004
C;Accession: S40357
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Birt. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
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C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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R;Cimanis, A.Y.
submitted to the EMBL Data Library, November 1993
A;Reference number: S38713
A;Accassion: S38719
A;Accassion: S38719
A;Molecule type: mRNA
A;Molecule type: MRNA
A;Coss.references: UNIPARC:UPI0000117543; EMBL:X760;
C;Superfamily: immunoglobulin V region; immunoglobuli
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 513; DB 2;
Pred. No. 1.5e-41;
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A,Status: preliminary; translation not shown
A,Redlecute type: mRNA
A,Residues: 1-136 <KLE>
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Best Local Similarity 86.6%;
Matches 97; Conservative
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Ig kappa chain V-II region TE33 - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 21-Jan-2000
C;Accession: A32967
R;Levy, R.; Assulin, O.; Scherf, T.; Levitt, M.; Anglister, J.
Biochemistry 28, 7168-7175, 1989
A;Title: Probing antibody diversity by 2D NMR: comparison of amino acid sequences, pred1 A;Reference number: A32967; MUID:90057406; PMID:2819059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
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                                                                                                                                                                                         21 DIVWIQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 80
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C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
                                                                                                                                                   1 DVVWTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
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R;Shefner, R.; Kleiner, G.; Turken, A.; Papazian, L.; Diamond, B.
D Exp. Med. 173, 287-286, 1991
A;Title: A novel class of anti-DNA antibodies identified in BALB/c mice.
A;Reference number: PT0352; MUID:91108325; PMID:1988536
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Best Local Similarity 84.8%; Pred. No. 3.7e-41;

Matches 95; Conservative 9; Mismatches 8; Indels
   Length 136;
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C;Comment: This protein is an anti-double-stranded DNA antibody.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;19-98/Domain: immunoglobulin homology <IMM>
                                                                     12; Indels
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86.2%; Score 513; DB 2;
86.6%; Pred. No. 1.8e-41;
iive 3; Mismatches 12;
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A,Reference number: A91043; MUID:86300658; PMID:2427335
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A, Residues: 1-112 <CAT.
A, Cross-references: UNIPROT: Q8VCI6; UNIPARC: UPI0000176A17
A, Experimental source: strain Balb/c
A, Note: this sequence was determined from the germline gene
C, Comment: This chain was isolated from a hybridoma protein that binds influenza virus h
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J. Biol. Chem. 265, 133-138, 1990
J. Biol. Chem. 265, 133-138, 1990
A;fitle: Active site structure and antigen binding properties of idiotypically cross-res A;Reference number: A34903; WUID:90094387; PMID:2104617
A;Accession: C34904
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A;Molecule type: mRNA
A;Residues: 1-131 - ABD.
A;Residues: 1-131 - ABD.
A;Cross-references: UNIPROT: QBVCI6; UNIPARC: UDI00001767A8
B;Bedzyk, W.D.; Johnson, L.S.; Riordan, G.S.; Voss Jr., E.W.
A;Title: Comparison of variable region primary structures within an anti-fluorescein idi
A;Reference number: A31485; MUID:89109167; PMID:2492278
A;Accession: 131485
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C;Species: Wus musculus (house mouse)
C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 09-Jul-2004
C;Accession: C34904; I31485
                                                   Ig kappa chain V region (H37-82) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQRPGQSPELLIYKVSNRF
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83.9%; Pred. No. 9.9e-41;
ive 9; Mismatches 9; Indels
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                                                                                                                                          C, Accession: C27887

R; Caton, A.J; Brownlee, G.G.; Staudt, L.M.; Gerhard, W. EMBO J. S, 1377-1591, 1986

A; Title: Structural and functional implications of a res
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A;Residues: 20-52 <BE2>
A;Cross-references: UNIPARC:UPI00001767A9
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Best Local S
Matches 94
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                                                                                                                                                                                                                                                   RESULT 12
B34904
Ig kappa chain precursor V region (12-40 and 5-14) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jul-2000
C;Accesion: B34904, #134903
R;Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J; Biol. Chem. 265, 133-138, 1990
A;Tible. Active site structure and antigen binding properties of idiotypically cross-rea A;Reference number: A34904
A;Reference number: A34904
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A;Rocession: B34904
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A;Rocession: B34904
C;Residues: 1-131 ABED-A;Rocession: MulpaRc;UPI0000114FC8; GB:M32384; GB:J05237; GB:J05238; NID:g639656; C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heteroterramer; immunoglobulin
F;35-114/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig kappa chain V region (4-4-20) - mouse (fragment)
Ig kappa chain V region (4-4-20) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 31-0ul-1989 #sequence_revision 31-Jul-1989 #text_change 09-Jul-2004
C;Accession: B31485
R;Bedzyk, W.D.; Johnson, L.S.; Riordan, G.S.; Voss Jr., E.W.
J. Biol. Chem. 264, 1565-1569, 1989
A;Title: Comparison of variable region primary structures within an anti-fluorescein idi
A;Reference number: A31485; MUD:89109167; PMID:2492278
A;Accession: B31485
A;Accession: B31485
A;Accession: B31485
A;Accession: Preliminary
A;Molecule type: protein
A;Residues: 1-112 <BBD>
A;Accession: mumparcic, UNIPARC:UPI0000176AF8
C;Superfemily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IWM>
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9; Mismatches 8; Indels
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87.5%; Pred. No. 5.5e-46;
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Copyright (c) 1993 - 2006 Compugen Ltd.
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                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
Klobeck H.G., Solomon A., Zachau H.G.; "Contribution of human V kappa II germ-line genes to light-chain
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PIR; A01889; KZHUGM.
HISSP; Q99M37; 1131.
SMR; P06309; 5:117.
GO; GO:0005823; F:antigen binding; NAS.
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GO; GO:0006985; P:antigen binding; NAS.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003596; Ig_v.
SMART; SMO0406; IG_v.
PROSITE; PSS0835; IG LIKE; 1.
Immunoglobulin domain; Immunoglobulin V region; Signal.
                                                                Nature 309:73-76(1984).
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DISULFID
                                                                                                                                                                                                            removed.
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                                                                                                                                                                                                                                                                        This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED outstain the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6410.
                                                                                                               NUCLEOTIDE SEQUENCE.
MEDLINE=86041852; PubMed=2997711;
Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;
"Human immunoglobulin kappa light chain genes of subgroups II and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWSWTFGQGTKVEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              kappa chain V-II region RPMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.0%; Score 500; DB 1; Length 133;
84.8%; Pred. No. 3.3e-44;
ive 8; Mismatches 9; Indels
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01-JAN-1988 (Rel. 06, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ensembl; ENSGO000173758; Homo sapiens.
GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0005823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
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Framework-1.
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PIR, A01890; KZHURP.
HSSP, 099M37; 1191.
SMR; P06310; 21-133.
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By similari
                                                                                                                                                                                                                              Nucleic Acids Res. 13:6499-6513(1985)
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PROSITE; PS50835; IG LIKE; 1.
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nes 95; Conservative
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113
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P06309;
01-JAN-1988 (
01-JAN-1988 (
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Ig kappa chain V-II region GM607. Framework-1.

Complementarity-determining-1. Complementarity-determining-2.

Framework-2

1117 27 43 58 65 97 106 116

28 44 44 59 66 98 107

Complementarity-determining-3.

By similarity

Framework-4. Framework-3

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
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                                                                                                                                                                                     83.7%; Score 498; DB 1; Length 117;
85.7%; Pred. No. 4.5e-44;
ive 3; Mismatches 13; Indels
                                                                                                  117 AA; 12664 MW; 92C57DC719E558B1 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QBNEKO_HUMAN PRELIMINARY;
QBNEKO;
                                                                                                                                                                                                                                                                                                       96; Conservative
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Name=IGKV1-5;
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Ig kappa chain V-II region GM607 precursor (Fragment). Homo sapiens (Human). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

NUCLEOTIDE SEQUENCE. MEDLINE=84191506; PubMed=6325927;

NCBI\_TaxID=9606;

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HUMAN
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Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu. K., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Schwetz J., Myers R.M., Sutterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Gener than 15,000 full-length human and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Expressed human immunoglobulin kappa genes and their hypermutation."; Eur. J. Immunol. 23:3248-3262(1993).
EMBL; BC030814; AAH30814.1: -: mRNA
                                                                                                                                                                                                                                                                                                                                                                                           Huber C., Klobeck H.G., Zachau H.G.; "Ongoing V kappa-J kappa recombination after formation of a productive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "V kappa gene segments rearranged in chronic lymphocytic leukemia are distributed over a large portion of the V kappa locus and do not show somatic mutation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
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                                                                                                                                                                                                                                                                                                         Director MGC Project;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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1 Similarity 83.9%; Pred. No. 1.3e-43;
94; Conservative 6; Mismatches 12;
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PIR; S23638; S23638.

PIR; S40342; S34091.

PIR; S40347; S40357.

PIRSP; P01834; 1172.

SMR; Q908K0; 21-237.

INTERPO; IPR007110; Ig-like.

INTERPO; IPR003597; Ig_c1.

INTERPO; IPR003597; Ig_c1.

INTERPO; IPR003597; Ig_v.

Pfam; PF07654; C1-8et; I.

SMART; SM00460; IGV; 1.
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PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                kappa-J kappa coding joint.";
1r. J. Immunol. 22:1561-1565(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bur. J. Immunol. 23:391-397(1993)
                                                                                                                                                                                                                     and mouse cDNA sequences.
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TISSUE=Prostate;
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                                                                                                                                                                                                                                                                                                                                                                             PubMed=1601042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=8436174
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                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TEXTY WD., Page D.L., Kimura S., Isobe T., Osserman E.F., Glenner G.G.;
Glenner G.G.;
Structural identity of Bence Jones and amyloid fibril proteins in a patient with plasma cell dyscrasia and amyloidosis.";
J. Clin. Invest. 52:1276-1281(1973).
-I- MISCELLANEOUS: The major amyloid protein appears to be identical with the Bence Jones protein isolated from the same patient.
-I- MISCELLANEOUS: This protein was isolated from the surine of a patient with plasma cell dyscrasia and amyloidosis.
-I- MISCELLANEOUS: The C region of this chain has the INV (1,2)
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                                                                                                                                                                                                                                                                                                                                                                      Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
"Amino acid sequence of a kappa Bence Jones protein from a case
primary amyloidosis.";
Biochemistry 12:3763-3780(1973).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).
MEDLINE-73166638; PubMed-4700495;
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Immunoglobulin V region.
                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Homo sapiens (Human).
113 AA
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                                                                                                                                                                                                                                                                                                                                (BENCE-JONES PROTEIN TEW).
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SMR; P01617; 1-113.

GO:0005576; C:extracellular region; NAS GO; GO:0003823; F:antigen binding; NAS. GO; GO:0006955; P:immune response; NAS. InterPro; IPR007110; Ig-like.

InterPro; IPR003596; Ig-like.

SMART; SM00406; IGV; I.

PROSITE; PS50835; IG_LIKE; I.

Amyloid; Bence-Jones protein; Direct protein and anyloid; Bence-Jones protein.
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PRT;
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MEDLINE=74148480; PubMed=4596149;
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STANDARD;
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Best Local Similarity
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NUCLEOTIDE SEQUENCE.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=8436174;
Wagner S.D., Luzzatto L.;
"V kappa gene segments rearranged in chronic lymphocytic leukemia are distributed over a large portion of the V kappa locus and do not show
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SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMZALQAPITFGQGTRLEIK 112
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MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
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                                                                                                                                                                                                                                                                                                                                                  01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
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Eur. J. Immunol. 22:1561-1565(1992).
EmbL; ARO35034; AAD56270.1; -; mRNA.
PIR; B49002; B49002.
PIR; S23638; S23638.
PIR; S34094; S34094.
PIR; S34095; S34095.
HSSP; P01625; ILVE.
SMR; Q9UL80; 1-114.
                                                                                                                                                                                                                                                                                                        Created)
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Eur. J. Immunol. 23:391-397(1993)
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InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                             QULSO HUMAN PRELIMINARY;
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DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Erlandsson A.;
Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ884575; CAI56337.1; -; mRNA.
InterPro; IPR003599; Ig.
InterPro; IPR00310; Ig-like.
InterPro; IPR003596; Ig.
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115 AA; 12560 MW; E4D3BF3D63E88007 CRC64;
                               Last sequence update)
Last annotation update)
                      10-WAY-2005 (TrEWBLrel. 30, Last sequence upda 10-WAY-2005 (TrEWBLrel. 30, Last annotation up Kappa light chain variable region (Fragment). Name=IgG1 anti-TS1 VL;
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21-JUL-1986 (Rel. 01, Last sequence update)
11-MAY-2005 (Rel. 47, Last annotation update)
19 kappa chain V-II region 26-10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 AA
Created)
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MEDLINE=83178921; PubMed=6404298;
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NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PP07686; V-set; 1.
SMART; SM00409; IG; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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NUCLEOTIDE S
TISSUE=Lung;
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                                This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Altschul S.P., Zeeberg B. S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Blate N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haleh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
MISCELLANEOUS: This chain was isolated from an IgG2a hybridoma
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                                                                                                                 HSSP, Q99M37; 1191.
Ensembl; ENSWUSG0000055315; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
SWART; SM0406; IGV; 1.
PR051TE; PS50835; IG LIKE; 1.
PR051TE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Monoclonal antibody.
                                                                                                                                                                                                                               Complementarity-determining-1. 
Pramework-2.
                                                                                                                                                                                                                                                        Complementarity-determining-2.
                                                                                                                                                                                                                                                                    Framework-3.
Complementarity-determining-3.
                                                                                                                                                                                                                                                                                                                                                         Length 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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82.1%; Pred. No. 1.6e-42;
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By similarity.
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            protein that binds digoxin.
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01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QBTCD0_HUMAN PRELIMINARY;
Q8TCD0;
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54
61
102
112
93
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                                                                                                      PIR; A01914; KVMS26.
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                                                                                                                                                                                                                                                                                                                                113 AA;
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Matches 92; Conserv
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SEQUENCE
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Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and inftial analysis of more than 15,000 full-length human and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Klein R., Jaenichen R., Zachau H.G.; "Expressed human immunoglobulin kappa genes and their hypermutation."; Eur. J. Immunol. 23:3248-3262(1993).
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"The human immunoglobulin kappa locus. Characterization of the duplicated A regions." Eur. J. Immunol. 22:1023-1029(1992).
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
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PROSITE; PS50835, IG LIKE; 2.
PROSITE; PS0090; IG MHC; UNKNOWN 1.
Hypothetical protein; Immunoglobulin domain.
SEQUENCE 239 AA; 26235 MW; PACEDC3A3B03871D CRC64;
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Pred. No. 6.3e-42;
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:ive 12; Mismatches
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PIR; 822668, 822658.
PIR; 834095; 834095.
PIR; 840324; 840324.
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InterPro; IPR003597; Ig cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig v.
Pfam; PF07654; Cl-set; I.
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PIR; $42267; $42267.
PIR; $42268; $42268.
HSSP; P01834; 1172.
SMR; QBTCD0; 21-237.
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                                                                                                                                                                                                                                                                                                                                              PubMed=1598223;
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PubMed=8258341;
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Nausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A botheren M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
Brantein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bask S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunzarne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Sheychenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Beneration and initial analysis of more than 15,000 full-length human
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                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                            MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80.3%; Score 478; DB 2; Length 23 79.5%; Pred. No. 1.3e-41; ive 11; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.; Strausberg R.; Submitted (DRC-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BC065299; AAH63599.1; -; mRNA. HSSP; P01837; 1KCU. SWR; Q6P491; 21-237.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
SEQUENCE 239 AA; 26245 MW; CD7313DDFFD358B3 CRC64;
                           vo-JUL-2004 (TrEMBLrel. 27, Created)
No-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Nypothetical protein.
Homo sapiens (Human).
Bukaryota; Merarr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                         239 A.A.
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PROSITE; PS00290; IG MHC; UNKNOWN 1.
                         PRT;
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InterPro; IPR00310; Ig-11ke.
InterPro; IPR003597; Ig c1.
InterPro; IPR003096; Ig d1.
InterPro; IPR003896; Ig w.
Pfam; PR07654; C1-set; I.
SMART; SM00407; IG2; I.
SMART; SM00407; IG2; I.
                   QEP491 HUMAN PRELIMINARY;
QEP491;
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nes 89; Conservative
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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Alausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schemen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schemen C.M., Schuler G.D.,
Altschul S.F., Jozdan H., Moore T., Max S.I., Wang J., Haiseh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casvaint T.L., Scheetz T.E.,
A Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McZwan P.J., McKernan R.J., Malek J.A., Gunzarne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield X.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield A., Schein J.E., Jones S.J.M., Marra M.A.,
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                                                                                                                                                                                                      Name=IGKV1-5;
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 DIVWAQSPLSLSVTPGEPASISCRSSQSLLHSNGYNYFDWYLQKPGQSPQLLIYWGSNRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Lung;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79.4%; Score 472.5; DB 2; Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.

TISSUE-Lung;
Director MGC Project;
Submitted (UTU-2012) to the EMBL/GenBank/DDBJ databases.
EMBL; BC034142; AAH34142.1; -; mRNA.
HSSP; PO1837; 1KB5.
SMR; QEPIHG; 23-240.
A InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003596; Ig.
InterPro; IPR003596; Ig.
InterPro; IPR003596; Ig.
R InterPro; IPR003596; Ig.
R SMART; SM00409; IG61; 1.
SMART; SM00409; IG61; 1.
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PROSITE; PS00290; IG WHC; UNKNOWN 1.
SEQUENCE 240 AA; Z6234 MW; 188D4DD8BB781EC4 CRC64;
                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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5; Mismatches 15
240 AA
PRT;
                                                                   Created)
                                                            05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
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QEPIHE HUMAN PRELIMINARY;
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                                                                                                                                                                      IGKV1-5 protein.
                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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KV2A\_HUMAN

RESULT 11

RESULT 12

us-10-735-916a-61.rup

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Best Local Similarity
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                     NCBI_TaxID=10090;
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NON TER
SEQUENCE
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                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00406; IGV; 1.—PROSITE; PS50835; IG_LIKE; 1.
Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain; Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    $\tilde{\Ose{053VPB}}$ MOUSB PRELIMINARY; PRT; 112 AA.
$\tilde{053VPB}$
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Molecular basis of antibody formation.";
Naturwissenschaften 56:195-205(1969).
-!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
-!- MISCELLANEOUS: This is a Bence-Jones protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHS-NGNTYLQWYLQKPGQSPQLLIYKVSNR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 LYGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 ASGVPDRFSGSGSGTDFTLKISRVQAEDVGVYYCMQRLEIPYTFGQGTKLEIR 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 AA; 12676 MW; 59E9F90A379569EC CRC64;
                                                                                                                                                                                                                                                                                                                                                      Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967)
                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Ig kappa chain V-II region Cum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSRP, P01751; INQB.
SMR; P01614; 2-115.
GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
  115 AA
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                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE REVISION TO 50; 52; 96 AND 97.
MEDLINE=70063440; Pubmed=4188189;
                                                                                                                                                                                                                                                                    MEDLINE=68242259; PubMed=5586923;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 79.6
nes 90; Conservative
  STANDARD;
                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; B91639; K2HUCM.
                                                                                                                                                                                                                                              PROTEIN SEQUENCE.
                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                     Hilschmann N.;
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KV2A HUMAN
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                                                                                                                                                                                                                                                                                                                                type)."
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ID AC Q5
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A MEDIANES/SOLISON; FUDNEGES BY 0.800.;

A KIDD B. Schladk M., Becker W.W.;

"Cloning and expression of a recombinant mouse Fab-fragment recognizating a defined linear epitope of Chironomus thummi thummi major at allergen Chi t. I., if allergen Chi t. I., if allergen Chi t. I., if Int. Arch. Allergy Immunol. 110:348-353(1996).

E Int. Arch. Allergy Immunol. 110:348-353(1996).

E REL, 237499; CAR85724.1; -; mRNA.

E REL, 237499; CAR85724.1; -; mRNA.

E REL, 27499; CAR85724.1; -; mRNA.

E REL, 27499; CAR85724.1; -; mRNA.

E REPPRO; IPR001359; IG. I.

E REPPRO; IPR001359; IG. I.

E REPPRO; IPR001359; IG. I.

E REPRO; IRR001359; IG. I.

E RAMRT; SM00409; IG. I.

E SWART; SM00409; IG. I.

E ROSITE; PS50835; IG. IIKE; 2.

E ROSITE; PS50835; IG. IIKE; 2.

E ROSITE; PS50835; IG. IKE; 2.
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NUCLECTIDE SEQUENCE.
MEDILINE=86136012; PubMed=3937730;
MEDILINE=86136012; PubMed=3937730;
Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
The idiotypic network and the internal image: possible regulation of
a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
antibodies in the GAT system.";
EMBO J. 4:3681-3688(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGIYYCFQGIHVPYTFGGGTRLEIK 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               79.0%; Score 470; DB 2; Length 112; 79.5%; Pred. No. 3.7e-41; ive 11; Mismatches 12; Indels
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                                                                                                                                                                                                                                                               Fougereau M.;
Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
EMBL; X03386; CAA27113.1; -; mRNA.
NON TER
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Last annotation update)
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Pred. No. 2.1e-40;
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STRAIN=Balb/c; TISSUE=Spleen;
MEDLINE=96319505; PubMed=8768802;
                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE OF 108-109.
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Q6SZCO;
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219 AA;
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                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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 Gaps
                                                                                                                                                                                                                                                                                                                                                                                   Riesen W.F., Jaton J.-C.;
"Variable region sequence of the light chain from a Waldenstroms IgM with specificity for phosphorylcholine.";
Biochemistry 15:3829-3833(1976).
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                                                                                -i- MISCELLANEOUS: This chain was isolated from a Waldenstrom's macroglobulin that binds phosphorylcholine.
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Complementarity-determining-3.
Framework-4.
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12; Indels
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PROSITE; PSS0835; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region.
                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
19 kappa chain V-II region FR.
Homo sapiens (Human).
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SMR; P01615; 1-109.
G0; G0:0005576; C:extracellular region; NAS.
G0; G0:0003823; F:antigen binding; NAS.
G0; G0:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR00356; Ig-v.
 11; Mismatches
                                                                                                                                                                                  113 AA.
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MEDLINE=76253627; PubMed=821524;
89; Conservative
                                                                                                                                                                                  STANDARD;
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54
61
102
112
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SEQUENCE
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Db 61 SGVPDRFSDSGSGTDFTLKITRVQAEDVGVYYCMQATZSPYTFGQGTKLZIK 112
Search completed: January 10, 2006, 20:53:25
Job time: 75.5025 secs
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January 10, 2006, 20:07:41; Search time 77.3134 Seconds (without alignments) 636.505 Million cell updates/sec
                                                                                                                                                                                                                                  1 DVVMTQSPLSLPVTPGEPAS......CFQGSHVPWTFGQGTKVEIK 112
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GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                    2443163 segs, 439378781 residues
                                                                           - protein search, using sw model
                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                    seq length: 0
seq length: 200000000
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                  Copyright
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Maximum DB
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geneseqp2000s:\* geneseqp2001s:\* geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Adj76895 Anti-IGF-Adz67065 Human ant Adj76899 Anti-IGF-Adz67069 Human ant Adj76899 Anti-IGF-Adz67069 Human ant Adj84950 Variable Adz67071 Human ant Adj84950 Variable Adp84950 Variable Adj84950 Variable Adj84960 Variable Mouse mon Mouse mon Mouse mon FGF-8 rel Humanised Humanised Description AAE15713 AAE15712 ADP84948 ADP84951 ADE36530 ADP84949 ADJ76899 ADZ67069 ADJ76901 ADZ67071 ADZ67071 AAY42969 ADP84944 ADJ76895 ADZ67065 ADJ76897 ADZ67067 AAE15711 ABP72125 ADP84946 ADE36523 ADE36495 ADP84947 8 Query Match Length 100.00 10 Result No.

Abp72129 FGF-8 rel	Ade36520 Anti-FGF-	Adv67310 Amino aci	Aar32239 Humanised	Aaw27145 Mature li	Aay87571 Humanised		Adp84945 Variable	Adp84952 Variable	Ade36518 Anti-FGF-	Adp84943 Variable	Adj80420 Hybrid hu		Abr40272 Amino aci		Adz52552 Anti-CCR4	Abr40268 Amino aci	Ade27687 Humanised	Ade36519 Anti-FGF-	Ade36527 Anti-FGF-	Adj80422 Murine an	
5 ABP72129	7 ADE36520	9 ADV67310	2 AAR32239	2 AAW27145	3 AAY87571	7 ADE36522	B ADP84945	8 ADP84952	7 ADE36518	8 ADP84943	7 ADJ80420	7 ADH61998	6 ABR40272	7 ADE27694	9 ADZ52552	6 ABR40268	7 ADE27687	7 ADE36519	7 ADE36527	7 ADJ80422	
112 6	112	112	112 2	112	112	112	114	114	112	114	112	132	112 (	112	112	112	112	112	112	112	
93.6	93.6	93.6	93.4	93.4	93.4	93.4	93.4	93.3	92.9	92.8	92.4	92.4	91.9	91.9	91.9	91.8	91.8	91.8	91.8	91.8	
557	557	557	556	556	556	556	556	555	553	552	550	550	547	547	547	546	546	546	546	546	
25	5.5	27	78	5 6	30	31	32	100	34	35	36	37	30	66	40	41	42	4.3	4	45	

## ALIGNMENTS

RESULT

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:\* geneseqp1990s:\*

A Geneseq 21:\*

Database :

insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region; cytostatic; antipsoriatic; antibody; (FABR ) FABRE MEDICAMENT SA PIERRE. ADJ76895 standard; protein; 112 AA Anti-IGF-1R related protein #12. Leger 0; 18-JAN-2002; 2002FR-0000653. 18-JAN-2002; 2002FR-0000654. 07-MAY-2002; 2002FR-0005753. 20-JAN-2003; 2003WO-FR000178 (first entry) Corvaia N, WO2003059951-A2 Homo sapiens. 06-MAY-2004 24-JUL-2003. Goetsch L, ADJ76895; ADJ76895 

WPI; 2003-569653/53

New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.

Disclosure; SEQ ID NO 61; 164pp; French

The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (BGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of

N-PSDB; ADZ67066.

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           transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF. IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; geniforurinary disease; osteosaxcoma; musculloskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; light chain variable region.
                                                                                                                                                                                        1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
                                                                                                                                                                                                            1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQXPGQSPQLLIXKVSNRL 60
                                                                                                                                                               Gaps
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these receptors with their ligands. Especially they inhibit
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Pred. No. 2.4e-43;
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100.0%; Score 595; D
Best Local Similarity 100.0%; Pred. No. 2.4
Matches 112; Conservative 0; Mismatches
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/note= "CDR3"
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94. .10
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CORVAIA N.
LEGER O.
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                                                                                                           Sequence 112 AA;
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07-MAY-2002;
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contraction of the transduction pathway of the signal mediated by the interaction of IGF1 or IGF2 with IGF1R and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended connecter, preferably IGF-dependent, especially IGF1 and/or IGF2.

Condition of indivit the transformation of normal cells into cells with tumoral capacity. The armsformation of normal cells into cells with tumoral capacity of EGF-dependent and/or HERZ/neu-dependent cells. [1] is useful for preparation of a medicament intended to inhibit the growth and/or the proliferation of tumor cells, preferably IGF-dependent, especially IGF-dependent and/or IGF2-dependent and/or IGF2-dependent and/or IGF2-dependent and/or IGF2-dependent cells. [1] is useful in the preparation of a medicament intended for prevention or for the treatment of cancer, where the cancer is chosen from prostate cancer, osteosarcoma, lung cancer, breast cancer, endometrial cancer or colon cancer. [1] is useful in preparation of a medicament intended for the preparation of a medicament intended for the prevention or for the intended for the specific targeting of a biologically active compound to calls expressing or overexpressing of illnesses induced by an order in vitro diagnosis of illnesses induced by an order or an order of illnesses induced by an order or an order or and or an order or and order orde
                                                                                                                                                                                                                                                                                    I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tyrosine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADS67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or connected with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of IGF-
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                                              Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
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                                                                                                                                                                                                                                                           relates to a novel isolated anti-insulin-like growth
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100.0%; Pred. No. 2.4e-43;
iive 0; Mismatches 0;
                                                                                                                                                                                                       Example 12; SEQ ID NO 61; 125pp; English.
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Matches 112; Conservative
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light chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-1R) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-1R. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Bapecially they inhibit transformation of tumor cells, to so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoms; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 DVVWTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 79
 ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                          New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human antibody 7C10 1 light chain variable region SEQ ID NO:63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein sequence used to generate the Ab of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 595; DB 7;
100.0%; Pred. No. 2.9e-43;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 63; 164pp; French.
                                                                                                                                                                                                                                                                    (FABR ) FABRE MEDICAMENT SA PIERRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADZ67067 standard; protein; 131 AA
                                                                                                                                                                                                                                                                                                       Goetsch L, Corvaia N, Leger O;
                                                                                                                                                                                           18-JAN-2002; 2002FR-00000653.
18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
                                                                                                                                                            20-JAN-2003; 2003WO-FR000178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                          WPI; 2003-569653/53
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 131 AA;
                                                                                     WO2003059951-A2
                                                     Homo sapiens.
                                                                                                                        24-JUL-2003
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The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tyrosine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or connected with a signal mediated by the interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin contractor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral consecuted to proper consecuted with inhibition of IGF2 and of consecuted with inhibition of the insulin contractor, preferably IGF-dependent and/or HER2/neu-dependent cells, preferably IGF-dependent, especially IGF1 and/or IGF2-dependent and/or EGF-dependent and/or E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          medicament intended for prevention or for the treatment of cancer, where the cancer is chosen from prostate cancer, osteosarcoma, lung cancer, breast cancer, endometrial cancer or colon cancer. (1) is useful in the preparation of a medicament intended for the prevention or for the treatment of psoriasis. (1) is useful in preparation of a medicament intended for the specific targeting of a biologically active compound to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Beck A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leger O, Duflos A, Haeuw J,
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                                                                                                                   l. .19
/note= "leader peptide"
                                                                        Location/Qualifiers
                                                                                                                                                                           .62
.-- "CDR1"
                                                                                                                                                                                                                                                                         74. .80
/note= "CDR2"
                                                                                                                                                                                                                                                                                                                                                      113. .121
/note= "CDR3"
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20-JAN-2003; 2003WO-FR000178
11-JUL-2003; 2003FR-00008538
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2002FR-00000654
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N-PSDB; ADZ67066.
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CORVAIA N.
LEGER O.
DUFLOS A.
HAEUW J.
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Homo sapiens.
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                                                                                                                   Peptide
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cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I) is useful for in vitro diagnosis of illnesses induced by an overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (I), which is optionally labeled. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                       79
                                                                                                                                                                                                                                                                                                                                                                                                                                     insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                          DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                                                                                                                                                               DVVWTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                                                                                                                                        Gaps
                                                                                                                                                                                                                                 YGVPDRFSGSGSGTDFTLKISRVBAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                              YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 131
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                                                                                                                                Length 131;
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                                                                                                                               Score 595; DB 9;
Pred. No. 2.9e-43;
                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic; antipsoriatic; antibody;
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                                                                                                                                                                                                                                                                                                                         ADJ76899 standard; protein; 112
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                                                                                                                               100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2002FR-00000653
                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                      Matches 112, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-569653/53
                                                                                                                               Query Match
Best Local Similarity
                                                                                                       Sequence 131 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2003059951-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                                                                RESULT
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                  also for treating psoriagis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-1R and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
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                                                                                                                                                                                                                                                                                                     prostate, lung, breast, endometrium and colon, also osteosarcoma, and
                                                                                                                                                                                                                                                                             1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                              YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                           YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
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                                                                                                                                                                       99.8%; Score 594; DB 7; Length 112; 99.1%; Pred. No. 3e-43;
                                                                                                                                                                                                                            0; Indels
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                                                                                                                                                                                                                            1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADZ67069 standard; protein; 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; 2002FR-0000653.
; 2002FR-0000654.
; 2002FR-00005753.
; 2003WO-FR000178.
; 2003FR-00008538.
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                                                                                                                                                                                                                         Matches 111; Conservative
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CORVAIA N.
LEGER O.
                                                                                                                                                                                                 Similarity
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                                                                                                                           Sequence 112 AA;
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11-JUL-2003;
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                                                                                                                                                                          Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                         cytostatic; antipsoriatic; antibody; IGF-1R; tyrosine kinase activity; insulin-11ke growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                              1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                             starting from a biological sample in which the abnormal presence, of IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (I), which is optionally labeled. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCPQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 YGVPDRRSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                     Query Match 99.8%; Score 594; DB 9; Length 112; Best Local Similarity 99.1%; Pred. No. 3e-43; Matches 111; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                              sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADJ76901 standard; protein; 131 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-IGF-1R related protein #15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JAN-2003; 2003WO-FR000178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JAN-2002; 2002FR-00000653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                  Sequence 112 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or creat diseases associated with hoverexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor EGFR) and/or with hoperactivity of signal transduction pathways mediated by interaction of hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of numor cells to tumor cells, inhibit growth and/or prostate, lung, breast, endometrium and colon, also osteosarcoma, and prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 594; DB 7; Length 131;
Pred. No. 3.5e-43;
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                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 67; 164pp; French
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/note= "leader peptide"
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                                                                                                       (FABR ) FABRE MEDICAMENT SA PIERRE.
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                                                                                                                                                                          Leger 0;
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/note= "CDR1"
74. .80
/note= "CDR2"
113. .121
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                                   2002FR-00005753
18-JAN-2002; 2002FR-00000654
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                                                                                                                                                                          Corvaia N,
                                                                                                                                                                                                                                WPI; 2003-569653/53.
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Best Local Similarity
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                                   07-MAY-2002;
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Mismatches

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Matches 111; Conservative

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receptor (IGF-IR) antibody (I) to its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tyrosine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal cyleration of the IGF-IR and/or EGRF, and/or connected with a hyperactivation of the IGF-IR and/or Connected with a hyperactivation of the IGF-W and/or EGRF, and/or of EGF with EGRR, where interaction of IGF or IGF2 with IGF-IR and/or of EGF with EGRR, where the administration of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells with tumoral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           character, preferably IGF-dependent, especially IGF1 and/or IGF2.

dependent and/or EGF-dependent, especially IGF1 and/or IGF2.

dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is useful for preparation of a medicament intended to inhibit the growth especially IGF2-dependent and/or EGF-dependent, especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is useful in the preparation of a medicament intended for prevention or for the treatment of cancer, where the cancer, especially IGF2-dependent and/or EGF dependent and/or EGF2-dependent and/or EGF3-dependent and/or EGF3-de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel isolated anti-insulin-like growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the biological sample winch (1), which is optionally labeled. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-and appecifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Duflos A, Haeuw J, Beck A;
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/note= "CDR3"
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2002FR-00005753.
2003WO-FR000178.
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N-PSDB; ADZ67070.
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CORVAIA N.
LEGER O.
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Length 131;

Score 594; DB 9; Pred. No. 3.5e-43;

99.8%;

Query Match Best Local Similarity

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This invention describes novel recognition molecules, especially antibodies that bind specifically to the Core-1 antigen. The recognition molecules are used to make constructs containing the framework regions that be separate, include and/or flank the specified sequences, especially where the framework regions are from the immunoglobulin [Ig] superfamily, protease inhibitors, lectins, helix-bundle proteins and/or lipocalins. Wost especially the framework regions are from antibodies, particularly the variable heavy chain (VH) and the variable light chain (VL) of human and/or murine origin. The constructs may also include a His or myc tag, is a single-chain antibody fragment, multibody, Fab fragment, fusion protein of an antibody fragment, with peptide or protein, and/or an Ig of types G, M, A, B or D and/or their subclasses. It may be human, humanised, murine or chimeric, e.g. IgM without the J chain. The additional sequences/structures in the constructs are Ig domains of various species, interacting or stabilising domains, signal sequences, fluctuated types, cytolytic agents, enzymes, immuno-modulators or effectors, MHC molecules, antigens, chelators for radioactive labels, liposomes, transmembrane domains, viruses and/or cells, specifically
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                                      79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recognition molecules, e.g. antibodies (and nucleic acids) that bind specifically to Core-1 antigens, useful for diagnosis, treatment and prevention of tumors and metastases.
                                                                                                                                                                                                                                                                                                                                                                                         antibody; Core-1 antigen; framework region; immunoglobulin superfamily; procease inhibitor; lectin; helix-bundle protein; lipocalin; variable heavy chain; WH; variable light chain; WL; vaccine; diagnosis; alleviation; treatment; tumour; breast; colon; stomach; pancreas; large/small intestine; ovary; cervix; lung; prostate; kidney; liver;
                                        20 DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                                                                 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                         80 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 131
                                                                                                                                                                                                                                                                                                                                                        Variable light chain VL fragment Karo24 SEQ ID NO 92.
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                                                                                                                                                                                                                                ADP84950 standard; protein; 114
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Christensen PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus.
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Chimeric.
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                   acid encoding them, and related vectors and host cells, are useful for prevention (e.g. as vaccine), diagnosis, alleviation, treatment, monitoring and/or secondary treatment of tumours (specifically of breast, colon, stomach, pancreas, large/small intestine, ovary, cervix, lung, prostate, kidney and/or liver) and/or metastases (particularly to liver), specifically where these are positive for the Cl antigen. The products of the invention provide simple, reliable and efficient detection of tumours. They are specific for carcinoma and show almost no binding to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse; humanised form; monoclonal antibody alpha 340; gene therapy; epidermal growth factor receptor; BGF; cancer; colorectal; lung; breast; gastric; ovarian; immune response; cytostatic; cell growth; apoptosis; inhibitor; mutant; mutein; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
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macrophages. The antibodies, also constructs containing them, nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCPQGSHVPYTFGQGTKVEIK 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse monoclonal antibody alpha 340 Vk region variant, 340VKd.
                                                                                                                                                                                                                                                                                                                                                                                                      Score 569; DB 8; Length 114;
Pred. No. 4.2e-41;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "Wild type Asn substituted with Lys"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "Wild type Leu substituted with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "Wild type Leu substituted with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      substituted with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE15713 standard; protein; 112 AA
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24-AUG-2000; 2000GB-00020794.
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                                                                                                                                                                                                                                                                                                                                                                                                            95.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                 Sequence 114 AA;
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                                                                                                                                                                                                                                                                                     healthy tissue.
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local 8
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The present invention relates to a humanised form of the antibody 340 (a mouse monoclonal antibody which binds to epidermal growth factor (EGF) receptor and inhibits binding of EGF), obtainable from the cell line of deposited with the ECACC under accession number 97021428. The humanised form of the antibody 340 is useful in gene therapy, medicine and in the manufacture of a medicament for treatment or prophylaxis of cancer. The invention is useful for treating colorectal, lung, breast, gastric or ovarian cancers or also for preventing the recurrence of cancer after initial treatment or surgery. The invention is also useful for enhancing a protective immune response against cancer by optimised immunisation conceptor, as the original murine antibody and has increased ability to immunogenicity but shows similar binding to cells expressing EGF receptor, as the original murine antibody and has increased ability to inhibit the growth and apoptosis inhibitor. The present sequence is mouse monoclonal antibody alpha 340 deimmunised light chain variable (VK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                New humanized form of mouse monoclonal antibody 340 which binds to epidermal growth factor receptor and inhibits binding of growth factor, useful for treating colorectal, lung, breast, gastric and ovarian cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse; humanised form; monoclonal antibody alpha 340; gene therapy; epidermal growth factor receptor; EGF; cancer; colorectal; lung; breast; gastric; ovarian; immune response; cytostatic; cell growth; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DVLMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLEWYLQKPGQSPQLLIYKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGVPDRFSGSGSGTDFTLKISRVEAEDVGIYYCFQGSHVPWTFGGGTKVEIK 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse monoclonal antibody alpha 340 Vk region variant, 340VKc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 568; DB 5; Length 112;
Pred. No. 5e-41;
3; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "Wild type Ser substituted with Thr"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inhibitor; mutant; mutein; variant.
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                                                                                                                                                                            Example 2; Fig 7; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.5%;
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                                  Durrant LG;
(SCAN-) SCANCELL LID.
                                                                  WPI; 2002-062384/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 112 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Variable light chain VL fragment Karoll SEQ ID NO 90.

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The present invention relates to a humanised form of the antibody 340 (a mouse monoclonal antibody which binds to epidermal growth factor (EGF) receptor and inhibits binding of EGF), obtainable from the cell line deposited with the ECACC under accession number 97021428. The humanised form of the antibody 340 is useful in gene therapy, medicine and in the manufacture of a medicament for treatment or prophylaxis of cancer. The invention is useful for treating colorectal, lung, breast, gastric or ovarian cancers or also for preventing the recurrence of cancer after initial treatment or surgery. The invention is also useful for enhancing a protective immune response against cancer by optimised immunisation acchedules. The humanised form of the antibody 340 has reduced immunogenicity but shows similar binding to cells expressing EGF receptor, as the original murine antibody and has increased ability to implie the growth of EGF receptor expressing cells. The invention is used as cell growth and apoptosis inhibitor. The present sequence is mouse monoclonal antibody alpha 340 deimmunised light chain variable (VK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New humanized form of mouse monoclonal antibody 340 which binds to epidermal growth factor receptor and inhibits binding of growth factor, useful for treating colorectal, lung, breast, gastric and ovarian cancer.
                                      "Wild type Lys substituted with Gln"
                                                                                                                                                                                               /note= "Wild type Asn substituted with Lys"
"Wild type Gln substituted with Pro"
                                                                                                                    note= "Wild type Ile substituted with
                                                                                                                                                        'note= "Wild type Leu substituted with
                                                                           "Wild type Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Fig 7; 53pp; English.
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24-AUG-2000; 2000GB-00020794
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ellis JRM, Durrant LG;
                                        note=
                                                                                 note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             region variant, 340VKc
                                                                                                                                                                                                                                                                                                                                                                                                                   (SCAN-) SCANCELL LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-062384/08.
                    Misc-difference
                                                         Misc-difference
                                                                                               Misc-difference
                                                                                                                                                                             Misc-difference
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                                                                                                                                        Misc-difference
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1 DVLMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLEWYLQXPGQSPQLLIYKVSNRF 60
                                                                               1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
                                        Gaps
                                                                                                                                                         61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCPOGSHVPWTFGOGTKVEIK 112
                                                                                                                                                                                 SGVPDRFSGSGSGTDFTLKISRVBAEDTGVYCFOGSHVPWTFGGGTKVBIK 112
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95.0%; Score 565; DB 5; Length 112; 94.6%; Pred. No. 9.1e-41; ive 2; Mismatches 4; Indels
                                        Conservative
                Similarity
                                    106;
  Query Match
                      Local
                                      Matches
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ADP84948 standard; protein; 114 AA
                                         ADP84948;
RESULT 12
         ADP84948
ID ADP8
XX
AC ADP8
XX
DT 09-S
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(first entry)

09-SEP-2004

This invention describes novel recognition molecules, especially antibodies that bind specifically to the Core-1 antigen. The recognition molecules are used to make constructs containing the framework regions that separate, include and/or flank the specified sequences, especially the teamework regions are from the immunoglobulin (Ig) superfamily, compretes inhibitors, lectins, helix-bundle proteins and/or lipocalins. Most especially the framework regions are from antibodies, particularly the variable heavy chain (VH) and the variable light chain (VL) of humans and/or muxine origin. The constructs may also include a His or myc tag, a clysine-rich region and/or a multimerisation domain, most particularly it is a single-chain antibody fragment, multibody, Pab fragment, fusion crypes G, M, A, E or D and/or their subclasses. It may be human, thumanised, mutine or chimeric, e.g. IgM without the J chain. The contines in the constructs are Ig domains of additional sequences/structures in the constructs or Ig domains of additional sequences/structures in the constructs or Ig domains of specificities, interacting or stabilising domains, signal sequences, corrects, MT collytic agents, enzymes, immuno-modulators or effectors, MT collotic agents, enzymes, immuno-modulators or constructs containing them, nucleic contained them, and related vectors and host cells, specifically or prevention (e.g. as vaccine), diagnosis, alleviation, treatment. antibody; Core-1 antigen; framework region; immunoglobulin superfamily; protease inhibitor; lectin; helix-bundle protein; lipocalin; variable heavy chain; VH; variable light chain; VL; vaccine; diagnosis; alleviation; treatment; tumour; breast; colon; stomach; pancreas; large/small intestine; ovary; cervix; lung; prostate; kidney; liver; New recognition molecules, e.g. antibodies (and nucleic acids) that k specifically to Core-1 antigens, useful for diagnosis, treatment and prevention of tumors and metastases. ä Stahn Danielczyk A, Karsten U, Ravn P, (NEMO-) NEMOD BIOTHERAPEUTICS GMBH & CO KG Claim 15; SEQ ID NO 90; 136pp; German. 01-DEC-2003; 2003WO-DE003994. 29-NOV-2002; 2002DE-01056900. WPI; 2004-461095/43. WO2004050707-A2 Christensen PA; Mus musculus sapiens metastasis. 17-JUN-2004 Goletz S, Chimeric. Ношо 

Gaps ö Length 114; Score 565; DB 8; Length 11: Pred. No. 9.2e-41; 4; Mismatches 2; Indels 95.0%; Query Match Best Local Similarity 94.6<sup>†</sup> Matches 106, Conservative Sequence 114 AA;

nealthy tissue.

prevention (e.g. as vaccine), diagnosis, alleviation, treatment, monitoring and/or secondary treatment of tumours (specifically of breast, colon, stomach, pancreas, large/small intestine, ovary, cervix, lung, prostate, kidney and/or liver) and/or metastases (particularly to liver), specifically where these are positive for the Cl antigen. The products of the invention provide simple, reliable and efficient detection of tumours. They are specific for carcinoma and efficient obinding to

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New humanized form of mouse monoclonal antibody 340 which binds to epidermal growth factor receptor and inhibits binding of growth factor, useful for treating colorectal, lung, breast, gastric and ovarian cancer.
                                                                                                                                                                                                                                                     Mouse; humanised form; monoclonal antibody alpha 340; gene therapy; epidermal growth factor receptor; EGF; cancer; colorectal; lung; breast; gastric; ovarian; immune response; cytostatic; cell growth; apoptosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a humanised form of the antibody 340 mouse monoclonal antibody which binds to epidermal growth factor (EGF)
61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                           SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPYTFGQGTKVEIK 112
                                                                                                                                                                                                                             Mouse monoclonal antibody alpha 340 VK region variant, 340VKb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Wild type Asp substituted with Glu"
                                                                                                                                                                                                                                                                                                                                                                                                 'note= "Wild type Thr substituted with Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "Wild type Lys substituted with Gln"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "Wild type Leu substituted with Thr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "Wild type Leu substituted with Val"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Wild type Asn substituted with Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "Wild type Leu substituted with Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "Wild type Ile substituted with Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note= "Wild type Gln substituted with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "Wild type Ile substituted with
                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "Wild type Ser substituted with
                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
7
                                                                                                                                                                                                                                                                                    gastric; ovarian; immune response;
inhibitor; mutant; mutein; variant
                                                                                                                                           AAE15711 standard; protein; 112 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-MAY-2000; 2000GB-00011981
24-AUG-2000; 2000GB-00020794
                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SCAN-) SCANCELL LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-062384/08.
                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
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                                                                                                                                                                                                                                                                                                                              Mus sp.
Synthetic.
                                                                                                                                                                       AAE15711;
                                                                                                                                                                                                                                                                                                                                                                        Key
                                                                                                                RESULT
AAE1571
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receptor and inhibits binding of EGF), obtainable from the cell line deposited with the ECACC under accession number 97021428. The humanised form of the antibody 340 is useful in gene therapy, medicine and in the manufacture of a medicament for treatment or prophylaxis of cancer. The invention is useful for treating colorectal, lung, breast, gastric or ovarian cancers or also for preventing the recurrence of cancer after initial treatment or surgery. The invention is also useful for enhancing contective immune response against cancer by optimised immunisation schedules. The humanised form of the antibody 340 has reduced immunogenicity but shows similar binding to cells expressing EGF receptor, as the original unwrine antibody and has increased ability to inhibit the growth of EGF receptor expressing cells. The invention is used as cell growth and apoptosis inhibitor. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to novel humanised antibodies and antibody fragments which react with fibroblast growth factor 8 (FGF8) and inhibit its biological functions. The polypeptides of the invention have cytostatic activity. The antibody is useful for the treatment of cancer, including prostate, breast, ovarian and testicular cancer. The present sequence is used in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                      1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Humanised antibodies and antibody fragments reacting with fibroblast growth factor 8 useful for the treatment and diagnosis of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Humanised; antibody; fibroblast growth factor 8; FGF8; cytostatic;
cancer; prostate; breast; ovarian; testicular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 YGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGVPDRFSGSGSGTDFTLKISRVEAEDTGVYYCFQGSHVPWTFGGGTKVEIK 112
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Pred. No. 1.3e-40;
3; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 19; Page 72; 86pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABP72125 standard; protein; 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FGF-8 related protein SEQ ID 17.
                                                                                                                                                                                                                                                                                                                                 94.6%;
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                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 93.8
Matches 105; Conservative
                                                                                                                                                                                                                                                          region variant, 340VKb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-239169/23.
                                                                                                                                                                                                                                                                                               Sequence 112 AA;
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Sequence 112 AA;

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Job time : 78.3134 secs
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                                                                               1 DVVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLQWYLQKPGQSPQLLIYKVSNRL 60
                                                                                                 The invention comprises a method for treating and preventing arthritis, the method involves the use of anti-FGF-8 (sic fibroblast growth factor) antibody. The antibody and method of the invention is useful for: the detection, treatment and prevention of arthritis; as a cartilage protection agent; as a joint destruction inhibitor; and as a synoviral proliferation inhibitor. The present amino acid sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treatment and prevention of arthritis comprising the use of anti-FGF-8 (sic fibroblast growth factor) antibody.
                                                                                                                                                                                                                                                                                                                                                             Anti-FGF-8 (sic fibroblast growth factor) antibody-related protein #2.
                                                Gaps
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                                                                                                                                             61 YGVPDRPSGSGSGTDFTLKISRVBAEDVGVYYCFQGSHVPWTFGQGTKVBIK 112
                                                                                                                                                                SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYCFQGSHVPYTFGQGTKVBIK 112
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                Length 112;
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                                               2; Indels
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               94.6%; Score 563; DB 6;
93.8%; Pred. No. 1.3e-40;
iive 5; Mismatches 2;
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94.6%; Score 563; DB 7;
Best Local Similarity 93.8%; Pred. No. 1.3e-40;
Matches 105; Conservative 5; Mismatches 2.
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                                                                                                                                                                                                                                                               ADE36495 standard; protein; 112 AA
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                                                                                                                                                                                                                                                                                                                             (first entry)
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                                Best Local Similarity 93.8
Matches 105; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified.
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                  Query Match
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Search completed: January 10, 2006, 20:44:14

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Sequence 54, Application US/11012353

Sequence 54, Application US/11012353

Publication No. US20050249730A1

GENERAL INFORMATION:
APPLICANT: CORVALA, NATHALIE
APPLICANT: CORVALA, NATHALIE
APPLICANT: HAEUW, JEAN-FRANCOIS
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
TILE REFERENCE: 017753-198
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT APPLICATION NUMBER: 10/735-916
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2002-01-08
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR SPLICATION NUMBER: FR 0200653
PRIOR FILING DATE: 2002-01-18
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        Sequence Sequence Sequence S
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100.0%; Pred. No. 1.1e-39;
tive 0; Mismatches 0;
US-10-932-334-58
US-10-932-334-62
US-10-932-334-62
US-10-932-334-65
US-10-932-334-65
US-10-932-334-64
US-10-932-334-94
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                Query Match
Best Local Similarity 100.
Matches 112; Conservative
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US-11-012-353-54
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1 DVLMTQIPLSLPVSLGDQAS......CFQGSHVPWTFGGGTKLEIK 112
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2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
                                                    GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd
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US-10-912-184-67
US-10-512-184-67
US-10-512-184-67
US-10-512-184-67
US-10-512-184-67
US-10-932-334-60
US-10-932-334-69
US-11-012-353-65
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Maximum Match 100%
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TYPE: PRT
ORGANISM: Mus musculus
US-11-125-837-23
                                                                                                                                        ORGANISM: Mus musculus US-11-012-353-56
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                                                                                                     LENGTH: 112
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                                   Sequence 56, Application US/11012353

Sequence 56, Application WS20050249730A1

GENERAL INPORMATION:
APPLICANT: GOETSCH, LILIANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: LEGER, OLIVIER
APPLICANT: ROWEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
TILLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
TILLE OF INVENTION: ROWER: US/1/1012,353
CURRENT APPLICATION NUMBER: US/1/1012,353
CURRENT FILING DATE: 2003-10-16
BRIOR FILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: PCT/FR03/00178
PRIOR FILING DATE: 2003-01-20
PRIOR FILING DATE: 2003-01-20
PRIOR FILING DATE: 2003-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQWYLQKPGQSPKLLIYKVSNRL 60
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              Sequence 49, Application US/11012353
Publication No. US20050249730A1
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20 DVLMTQTPLSLPVSLGDQASISCRSSQSIVNSNGNTYLEWYLQKPGQSPKLLIYKVSNRF 79
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US-11-089-266-66

Publication No. US20050287148A1

Sequence 66, Application No. US20050287148A1

GENERAL INFORMATION:

APPLICANT: Chatterjee, Malaya

APPLICANT: Chatterjee, Sunil K.

TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE

TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA

NUMBER OF SEQUENCES: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
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                                                                                                                                                                                                                                                                                    Query Match
95.6%; Score 564; DB 7; Length 112;
Best Local Similarity 95.5%; Pred. No. 1.1e-37;
Matches 107; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: FR 0200653
PRIOR PILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 0200654
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SCHWARE: Patentin Ver. 3.3
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Best Local Similarity 94.6
Matches 106; Conservative
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Sequence 15, Application US/11089266

Publication No. US20050287148A1

GENERAL INFORMATION:
APPLICANT: Chatterjee, Malaya
APPLICANT: Chatterjee, Malaya
APPLICANT: Chatterjee, Sunil K.
TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSER: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 93.4%; Score 551; DB 7; Length 263; Best Local Similarity 93.8%; Pred. No. 2.1e-36; Matches 105; Conservative 1; Mismatches 6; Indels
                                                                     CITY: PALO ALL.
STATE: CA
STATE: CA
COUNTRY: USA
ZIP: 94304-101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/11/089,266
FILING DATE: 23-Mar-2005
FILING DATE: 23-Mar-2005
FILING DATE: 23-Mar-2005
FILING DATE: 1999-04-15
APPLICATION NUMBER: US/01/153,401
FILING DATE: 1999-04-15
APPLICATION NUMBER: US 08/293,533
FILING DATE: 1999-04-15
APPLICATION NUMBER: US 08/591,196
FILING DATE: 1996-01-17
APPLICATION NUMBER: US 08/591,196
FILING DATE: 1996-01-16
ATTORNEY/AGENT INFORMATION:
NAME: CATHERINE M. POLIZZI
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 304142000202
TELEDROWNINICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: amino acid
                               E: MORRISON & FOER 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear; MOLECULE TYPE: protein US-11-089-266-66
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk

COMPATING SYSTEM: PC-D050/85-005

COMPATING SYSTEM: PC-D050/85-005

COMPATING SYSTEM: PC-D050/85-005

COMPATING SYSTEM: PC-D050/85-005

COMPATING SYSTEM: START START START SYSTEM SYSTEM
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                                                                                                                                                                                                                                                                                                                                                                  1 DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRF 60
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                                                                                                                                                                                                                                              Length 112;
                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 69 Application US/10932334
| Publication No. US20050249728A1 |
| GENERAL INFORMATION: US20050249728A1 |
| GENERAL INFORMATION: THE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY ITILE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY FILE REFERENCE: A6689 |
| CURRENT APPLICATION NUMBER: US/10/932,334 |
| CURRENT PILING DATE: 2004-09-02 |
| PRIOR APPLICATION NUMBER: US/10/729,441 |
| PRIOR PILING DATE: 2003-12-08 |
| PRIOR PILING DATE: 2003-06-14 |
| NUMBER OF SEQ ID NOS: 96 |
| SEQ TWARE: Patentin version 3.2 |
| LENGTH: 113 |
                                                                                                                                                                                                                                         Score 547; DB 7;
Pred. No. 2.2e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: synthetic antibody structure
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OTHER INFORMATION: "X" may be any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MISC FEATURE
1 LOCATION: (101)...(101)
2 OTHER INFORMATION: "X" may be any amino acid
US-10-932-334-69
                                                                                                                                                                                                                                         Query Match 92.7%; Score 547; DB Best Local Similarity 92.0%; Pred. No. 2.2e Matches 103; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                   PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARE: Patentin Ver. 3.3
SEQ ID NO 57
LENGTH: 112
PRIOR APPLICATION NUMBER: FR
                                                                                                                                          ; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-353-57
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US-11-089-266-2
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Sequence 2, Application US/11089266 Publication No. US20050287148A1 GENERAL INFORMATION:

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PAPICANT: Poon, Kenneth A.

APPLICANT: Poon, Kenneth A.

ITILE OF INVESTION: MONOCLOMAL ANTIBODY 1A7 AND USE FOR THE

TITLE OF INVESTION: PROMICABLA ANTIBODY 1A7 AND USE FOR THE

CORPERED MANESCA MONOCLOMAL ANTIBODY 1A7 AND USE FOR THE

CORPERED MANESCA MONOCLOMAL ANTIBODY 1A7 AND USE FOR THE

CORPERATION: TREATMENT OF MEMBERS OF A STATE O
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TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                     US-10-512-184-30
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LENGTH: 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 92.4%; Score 545; DB 7; Length 112; Best Local Similarity 92.9%; Pred. No. 3.1e-36; Matches 104; Conservative 3; Mismatches 5; Indels
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Publication No. US20050249728A1

GENERAL INPORMATION:

TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY

FILE REFERENCE: A8689

CURRENT APPLICATION NUMBER: US/10/932,334

CURRENT APPLICATION NUMBER: US/10/729,441

PRIOR PILING DATE: 2004-09-02

PRIOR FILING DATE: 2003-12-08

PRIOR FILING DATE: 2003-16-14

NUMBER OF SEQ ID NOS: 96

SOFTWARE: PATCHTING DATE: 2010-16-14

NUMBER OF SEQ ID NOS: 96

SEQ ID NO 61

LENGTH: 113
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              CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT FILING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: 10/735,916
PRIOR PILING DATE: 2003-12-16
PRIOR PILING DATE: 2003-12-16
PRIOR PLING DATE: 2003-01-11
PRIOR APPLICATION NUMBER: FR 0308538
PRIOR APPLICATION NUMBER: FR 020573
PRIOR PILING DATE: 2003-01-20
PRIOR PLING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 020653
PRIOR PLING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 020654
PRIOR PLING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
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Matches 103; Conservative
FILE REFERENCE: 017753-198
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Mus musculus
US-11-012-353-55
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US-10-932-334-61
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LENGTH: 112
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Sequence 67, Application US/10512184
Fublication No. US20050244901A1
GENERAL INFORMATION:
APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: Antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: Antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: resistance against fungi
FILE REPERENCE: 3381.010501
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SOSTWARE PATENTION OF: 2.1
Sequence 30, Application US/10512184
Publication No. US20050244901A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: Antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: resistance against fungi
FILE REFERENCE: 3581.01USO1
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT PILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PATENTIN VET. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: scFv VD2 with OTHER INFORMATION: specificity against Verticillium dahliae; OTHER INFORMATION: originates from Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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OTHER INFORMATION: Description of Artificial Sequence: precursor
OTHER INFORMATION: fusion protein comprising AG - linker - scFv VD2.
US-10-512-184-67
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Sequence 66, Application US/10512184
Publication No. US20050244901A1
GENERAL INFORMATION:
APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: resistance against fungi
TITLE OF INVENTION: resistance against fungi
FILE REFERENCE: 3881.014501
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 66
LENGTH: 569
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies, recombinant
TITLE OF INVENTION: Antibodies, recombinant
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: resistance against fungi
FILE REFERENCE: 3581.01US01
CURRENT PPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: PREDICT OF SEQ ID NOS: 72
SOFTWARE: PATENTIAL SEQUENCE
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US-10-512-184-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: precursor OTHER INFORMATION: fusion protein comprising chitinase - linker OTHER INFORMATION: SCFV VD2.
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92.0%; Score 543; DB 6;
Best Local Similarity 92.9%; Pred. No. 1.8e-35;
Matches 104; Conservative 2; Mismatches 6
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US-10-512-184-66
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Search completed: January 10, 2006, 21:36:22 Job time : 5.71144 secs

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1 DVLMTQIPLSLPVSLGDQAS......CFQGSHVPWTFGGGTKLEIK 112
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/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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US-08-324-131-2
US-08-253-533-66
US-08-752-844-15
US-08-253-151-15
US-08-251-136-15
US-08-251-136-2
US-08-591-136-2
US-08-591-136-2
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US-08-331-398A-67
US-08-331-398A-67
US-08-331-398A-67
US-08-331-398A-67
US-08-331-398A-67
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US-09-196-522-190
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US-08-859-649-19
US-08-207-861-19
US-08-207-861-29
US-08-859-648-19
US-09-192-545-4
US-09-192-545-4
US-09-331-398A-48
US-08-331-398A-48
US-08-077-2528-3
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Maximum Match 100%
Listing first 45 summaries
                                                                                                            - protein search, using sw model
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RESULT 2
US-09-324-191-2
i Sequence 2. Application US/09324191
Fatent No. 6562798
GENERAL INFORMATION:
APPLICANT: THE UNIVERSITY OF KENTUCKY RESEARCH FOUNDATION
APPLICANT: THE UNIVERSITY OF KENTUCKY RESEARCH FOUNDATION
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF PSORIASIS
FILE REFERENCE: 30414200540
CURRENT FILING DATE: 1999-06-02
SCHRENT FILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATCHLIN Ver. 2.0
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Sequence 2, Application US/09192838B

Setent No. 635244

GENERAL INFORMATION:
APPLICANT: PRON, KENNET A.

APPLICANT: CHATTERJEE, Malaya

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TRATMENT OF PSORIASIS
FILE REPRENSE: 30414200050

CURRENT APPLICATION NUMBER: US/09/192,838B

CURRENT FILING DATE: 1998-11-16

PRIOR APPLICATION NUMBER: 60/065,774

PRIOR PILING DATE: 1997-11-17

NUMBER OF SEQ ID NOS: 5

SOFTHARE: PATENTIN VOS: 2.0
                                      Sequence 3, Appli
Sequence 48, Appli
Sequence 3, Appli
Sequence 34, Appli
Sequence 34, Appl
Sequence 34, Appl
Sequence 34, Appli
Sequence 5, Appli
Sequence 9, Appli
Sequence 27, Appli
Sequence 27, Appli
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US-08-331-397B-48
US-08-759-804A-48
US-09-002-753A-3
US-09-27-693-48
US-08-657-274-3
PCT-US94-06687-3
US-08-227-693-34
US-08-331-398A-34
US-08-331-398A-34
US-08-311-398A-34
US-08-3171-9
US-08-053-171-9
US-10-226-795-27
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US-10-226-795-27
US-09-254-180C-183
US-09-254-180C-183
US-09-254-180C-183
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US-09-254-180C-183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-192-838B-2
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RESULT 4
US-09-293-533-66
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                                                                                                                                                                                                                          1 DVLATQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 66, Application US/08752844

Patent No. 593881

Patent No. 593881

GENERAL INFORMATION:

APPLICANT: Chatterjee, Malaya

CONFERT: Chatterjee, Malaya

STREET: 755 PAGE MILL ROAD

CITY: PALO ALTO

STATE: Chatterjee, Malaya

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: BA PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

PATENT CATION NUMBER: US/08/752,844
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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                                                                                                                                                                                                                                                                                                                   61 YGVPDRFSGSGSGTDFTLKISSVRAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                      80 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCRQGSHVPWTFGGGTKLEIK 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.4%; Score 551; DB 1; Length 263; 93.8%; Pred. No. 1.4e-45; Live 1; Mismatches 6; Indels
                                                                                                                                   Length 149;
                                                                                                                              Query Match 93.4%; Score 551; DB 2; Length 14; Best Local Similarity 93.8%; Pred. No. 7.6e-46; Matches 105; Conservative 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30414-20002.21
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FILING DATE:
FLING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SCHIEF, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 3041
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEPHONE: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELDEAN: (412)
TELEFAX: 706141
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 93.8
Matches 105; Conservative
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MOLECULE TYPE: protein
                                          t TYPE: PRT
COGANISM: Mus Musculus
US-09-324-191-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-752-844-66
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                       LENGTH: 149
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SEQ ID NO 2
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152 DVLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPNLLIYFVSNRF 211
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Patent No. 6509016
| Patent No. 6509016
| Patent No. 6509016
| GENERAL INFORMATION:
| APPLICANT: Chatterjee, Malaya |
| APPLICANT: Chatterjee, Malaya |
| APPLICANT: Chatterjee, Malaya |
| APPLICANT: Chatterjee, Sunil K. |
| TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA |
| NUMBER OF SEQUENCES 66 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: MORRISON & FOERSTER |
| STREET: 755 PAGE MILL ROAD |
| CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Chatterjee, Malaya
APPLICANT: Foon, Kenneth A.
APPLICANT: Foon, Kenneth A.
APPLICANT: Chatterjee, Sunil K.
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 93.4%; Score 551; DB 2; Length 263; Best Local Similarity 93.8%; Pred. No. 1.4e-45; Matches 105; Conservative 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                       STATE: CA
COUNTRY: USA
ZUP: 94304-1018
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/293,533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/752,844
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: SCHIff, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 30414-20002.21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-752-844-15; Sequence 15, Application US/08752844; Patent No. 5935821; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELERAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 66:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 263 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-09-293-533-66
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-591-196-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-293-533-15
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| Patent No. 2977316
| Patent No. Sequence No. Kenneth A. Applicant: Foon, Kenneth A. Applicant: Foon, Kenneth A. Applicant: Foon, Kenneth A. Applicant: Chatterjee, Sunil K. ITLE OF INVENTION: TREATMENT OF MELANOWA AND SMALL CELL CARCINOMA NUMBER OF SEQUENCES: 57
| CORRESPONDENCE ADDRESS: ADDRESSE: MORRISON & FOORESTER STREET: 755 PAGE MILL ROAD CITY: PALO ALTO
| CITY: PALO ALTO COUNTY: USA STATE: CA COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: Eloppy disk COMPUTER: Eloppy disk COMPUTER: Datentin Release #1.0, Version #1.30 CURRENT APPLICATION NUMBER: US/08/591,196 FILING DATE: 16-JAN-1996 FILING DATE: 16-JAN-1996 FILING DATE: 16-JAN-1996 FILING DATE: 16-JAN-1996 FILING DATE: 18-DAN-180-ANDESSE DATES APPRICATION NUMBER: US/ONE APPRICATION NUMBER: US/O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DVLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKKGQSPKLLIYFVSNRF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL 60
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                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30414-20002.21
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SCALIf, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 30414
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEPROX: (415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 494-0792
TELEX: 706141
INPORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS: LENGTH: 112 amino acide TYPE: amino acide STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-752-844-15
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1 DVLMIQTELSLPVSLGDQASISCRSSQSIVHSNGNIYLEWYLQKKGQSPKLLIYFVSNRF 60
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Patent No. 6509016

GENERAL INFORMATION:

APPLICANT: Chatterjee, Malaya
APPLICANT: Chatterjee, Malaya
APPLICANT: Chatterjee, Sunil K.

TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TITLE OF INVENTION: TREATMENT OF MELANOWA AND SMALL CELL CARCINOWA
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 92.9%; Score 548; DB 1; Length 112; Best Local Similarity 93.8%; Pred. No. 1.1e-45; Matches 105; Conservative 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/293,533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/752,844
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 30414-20002.21
TELEPHONE: (415) 813-5600
TELEPHONE: (415) 494-0792
                                                         30414-20002.20
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,253
REPERNICE/DOCKET NUMBER: 3041
TELECOMUNICATION INFORMATION:
TELEFAX: (415) 813-560
TELEFAX: (415) 494-0792
TELEFAX: 706141
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 112 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
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                                                                                                                                                                                   1 DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOS-152-844-2

JOS-152-844-2

JOS-152-844-2

Patent No. 5935821

GENERAL INPORMATION:

APPLICANT: Chatterjee, Malaya

APPLICANTON: TREATMENT OF MELANOWA AND USE FOR THE

TITLE OF INVENTION: MONOCIONAL AND SWALL CELL CARCINOMA

NUMBER OF SEQUENCES: 66

CORRESSONERCE ADDRESS:

ACOUNTY: PALO ALTO

STREET: 755 PAGE MILL ROAD

CONTYR: USA

STREET: ASA ASA ASTA AND

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

COMPUTER: PATENTIN RESTERM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/752,844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 DVFMTQTPLSLPVSLGDQASISCRSSQSIVASNGNTYLEWYLQKPGQSPNLLIYFVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                      61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                 61 SCVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
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                                                                                                                                   ò
                                                                                Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92.7%; Score 547; DB 1; Length 14
92.9%; Pred. No. 1.8e-45;
ive 1; Mismatches 7; Indels
                                                                                                                                6; Indels
                                                                             Score 548; DB 2;
Pred. No. 1.1e-45;
1; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30414-20002.21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 30414
TELEPHONE: (415) 813-5600
TELEPHONE: (415) 813-5600
TELEPHONE: (415) 494-0792
TELERX: 706141
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTER.STICS:
LENGTH: 149 amino acide
TYPE: amino acide
                                                                             92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 92.9
Matches 104; Conservative
                                                                                                                                Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
MOLECULE TYPE: peptide
                                                                             Query Match
Best Local Similarity
          ; MOLECOLE ...
US-09-293-533-15
                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
US-08-752-844-2
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RESULT 9

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| Program | Prog
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Score 545; DB 1;
Pred. No. 2.1e-45;
1; Mismatches 7;
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United States of America
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: WORDER: 5.1/5.2
CURRENT APPLICATION NUMBER: 13/041
RECISTRATION NUMBER: 33,041
RECISTRATION NUMBER: 33,041
RECISTRATION NUMBER: 33,041
TELEPHONE: (801) 532-1922
TELEPHONE: (801) 531-1926
INFORMATION FOR SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Utah
COUNTRY: United States of America
TELECOMMUNICATION INFORMATION:
                                                           TELEX: 388961 1PM04UT
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 annino acids
                                                                                                                                                                                                                                                                                                           n
Similarity 92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 114 amino acids
                       : 801/532-1922
801/531-9168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 92.4
Best Local Similarity 92.9
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 92.9
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                               unknown
                                                                                                                                                     amino acid
                                                                                                                                                     TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                          , HYPOTHETICAL:
US-08-497-312-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
US-08-560-558B-27
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                                           TELEPAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Method for obtaining modified immunogenicity of murine immunoglobulins with reduced immunogenicity of murine antibody variable domains, compositions containing them.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 DVFWTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEMYLQKPGQSPNLLIYFVSNRF 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 SGVPDRPSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 547; DB 2; Length 149;
Pred. No. 1.8e-45;
1; Mismatches 7; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATE: 30-JUN-1995
FILING DATE: 30-JUN-1995
                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/293,533
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/752,844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Method for obtaining modifit
TITLE OF INVENTION: immunoglobulins with reduce
TITLE OF INVENTION: antibody variable domains,
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: CENTRO DE INMUNOLOGIA MOLECULAR
STREET: 215 Y 15, ATABEY PLAYA
CITY: HAVANA
                                                                                                                                                                                                                          APPLICATION:
FILING DATE:
ATORING DATE:
ATORING SCHIff, J. Michael
REGISTRATION NUMBER: 40,253
REFRENCE/DOCKET NUMBER: 30414-20002.21
TELEPHONE: (415) 813-5600
TELEPHONE: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: BOND, LAURENCE B.
REGISTRATION NUMBER: 30,549
REFERENCE/DOCKET NUMBER: 2629US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18, Application US/08497312
Patent No. 5712120
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: CU 80/94
FILING DATE: 30-UN-1994
ATTORNEY/AGENT INFORMATION:
NAME: BOND. LAURENEY R
                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 706141
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: IENGTH: 149 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 92.7%;
Best Local Similarity 92.9%;
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
    COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-497-312-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-293-533-2
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Sequence 27, Application US/08560558E
; Sequence 27, Application US/08560558E
; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Humanized and chimeric monoclonal
TITLE OF INVENTION: antibodies that recognize epidermal growth factor receptor;
TITLE OF INVENTION: ESF-R); diagnostic and therapeutic use.
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Allen C. Turner, TRASK, BRITT & ROSSA
STREET: P.O. Box 2226
CITY: Salt Lake City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                             1 DVIATQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL 60
                                                                                                                                                     1 DVLMTQIPLSLPVSLGDQASISCRSSQNIVHSNGNTYLDMYLQKPGQSPNLLIYKVSNRF 60
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                                                      Gaps
                                                                                                                                                                                                                                    61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                           61 SGVPDRFRGSGSGTDFTLKISRVEAEDLGVYYCFQYSHVPWTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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Length 113;
                                                      7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DVLMTQIPLSLPVSLGDQASISCRSSQNIVHSNGNTYLDWYLQKPGQSPNLLIYKVSNRF 60
DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                    61 SGVPDRFRGSGSGTDFTLKISRVEAEDLGVYYCFQYSHVPWTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                  APPLICANT: Paten, Ira
APPLICANT: Willingham, Mark
APPLICANT: Willingham, Mark
APPLICANT: Willingham, Mark
APPLICANT: Willingham, Unich
APPLICANT: Brinkmann, Ulrich
APPLICANT: Germann, Ulrich
APPLICANT: California
COUNTRY: USA
                                                                                            61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Mouse monoclonal antibody B5 Light chain region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: BAETHIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,398A
FILING DATE: 28-CT-1994
FILING DATE: 30-SEP-1991
PRIOR APPLICATION NUMBER: US 07/767,331
FILING DATE: 12-CT-1990
ATTORNEY/AGENT INFORMATION:
NAME: HUMLEY: TOW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       015280-126110US
                                                                                                                                                                                                                                               Sequence 67, Application US/08331398A
Patent No. 5608039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 125 amino acids
amino acid
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Region
COCATION: 1..125
OTHER INFORMATION:
OTHER INFORMATION:
US-08-331-398A-67
                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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US-08-331-398A-67
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APPLICANT: Pastan, Ira
APPLICANT: Benhar, Ital
TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
TITLE OF INVENTION: Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DVLLIQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIXKVSNRF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL 60
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61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPFTFGSGTKLEIK 112
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Light chain region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER FRADABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURSKIT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,397B
FILING DATE: 28-OCT 1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 10-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATFORNEY AGENT INPORMATION:
NAME: HULLER: TOM
REGISTRATION NUMBER: 38,498
REGISTRATION NUMBER: 015280-126120US
TELEPHAN: (415) 543-9600
TELEFRAX: (415) 543-9600
TELEFRAX: (415) 543-5043
INPORMATION FOR SEQ ID NO:
ENVOYED: ALLO COMPANIED ACIDS
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ENVOYED: ALLO COMPANIEN ACIDS
INFORMATION FOR SEQ ID NO:
ENVOYED: ALL
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                       ; Sequence 67, Application US/08331397B; Patent No. 5981726; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 125 amino acids TYPE: amino acid
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Matches 104; Conservative
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OTHER INFORMATION: 1
US-08-331-3978-67
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US-08-331-397B-67
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US-08-759-804A-66

Sequence 66, Application US/08729804A

Patent No. 5990256

STREAL INFORMATION: Ration as ward

APPLICANT: Ration and Townsand and Crew Lip

STREET: Two Emberaced and Townsand and Crew Lip

STREET: Ward Emberaced and Townsand and Crew Lip

STREAT APPLICATION NUMBER: US 09/131.398

FILLING DATE: 30-522-1991

APPLICATION NUMBER: US 09/150/131

PRIOR APPLICATION NUMBER: 13.762

MARKER: Ward Emberaced And Marker Lib STR-0200

TTELEROWENE: Claim And Crew Lib Street Lib APPLICATION NUMBER: 13.762

STREET: WARD LIP CREW Embers: Claim And Crew Lib Street Lib APPLICATION NUMBER: 13.762

STREET: WARD LIP CREW Embers: Claim And Crew Lib Crew Mouse monoclonal antibody B5 Pv

OWEN MARCH

STREET: WARD LIB TOWN NUMBER: 13.762

OWEN MARCH

WARD LIB TOWN NUMBER: 13.762

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Search completed: January 10, 2006, 20:58:02 Job time : 22.8706 secs

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61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
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US-10-735-916A-49
Sequence 49, Application US/10735916A
Publication No. US20050084906A1
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57, Appl
69, Appl
2, Appl
84, Appl
85, Appl
86, Appl
16, Appl
61, Appl
61, Appl
110, Ap
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Sequence 190,
Sequence 190,
Sequence 29,
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1 DVIANTQIPLSLPVSLGDQAS.......CRQGSHVPWTFGGGTKLEIK 112
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Sequence 5
Sequence 1
Sequence 6
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                 1867569 seqs, 417829326 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                              - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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Sequence 4, Appli
Sequence 75, Appl
Sequence 17, Appl
Sequence 59, Appl
Sequence 59, Appl
Sequence 75, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 27, Appl
Sequence 117, Appl
Sequence 117, Appl
Sequence 112, Appl
Sequence 61, Appl
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   Sequence 60, A
Sequence 6, Ap
Sequence 4, Ap
Sequence 17, A
Sequence 4, Ap
Sequence 4, Ap
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CORVAIA, Nathalie
APPLICANT: CORVAIA, Nathalie
APPLICANT: LEGER, Olivier
APPLICANT: DUFLOS, Alain
APPLICANT: DUFLOS, Alain
APPLICANT: HAEUW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-183
CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT APPLICATION NUMBER: PR 03/08 538
PRIOR APPLICATION NUMBER: PR 03/08 538
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-01-16
PRIOR APPLICATION NUMBER: FR 02/00 653
PRIOR APPLICATION NUMBER: FR 02/00 654
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR SPUING DATE: 2002-01-18
PRIOR SEQ ID NOS: 156
SOFTWARE: PATENTIN VOIC: 2.1
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ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 54, Application US/10735916A Publication No. US20050084906A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Mus musculus
US-10-735-916A-54
                                     9911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.099111.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.099111.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.099111.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.099111.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.099111.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09911.09
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GENERAL INFORMATION:

APPLICANT: GOETSCH, Liliane

APPLICANT: CORVAIA, Nathalie

APPLICANT: CORVAIA, Nathalie

APPLICANT: CORVAIA, Nathalie

APPLICANT: BECK, Alain

APPLICANT: BECK, Alain

APPLICANT: BECK, Alain

APPLICANT: HABUW, Jean-Francois

TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF

FILE REFERENCE: 01753-183

CURRENT APPLICATION NUMBER: US/10/735,916A

CURRENT FILING DATE: 2003-07-11

PRIOR PILING DATE: 2003-07-11

PRIOR PILING DATE: 2003-07-11

PRIOR PILING DATE: 2003-01-18

PRIOR PILING DATE: 2002-01-18

PRIOR PILING DATE: 2002-05-07

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61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
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Pred. No. 1.1e-46;
1; Mismatches 4; Indels
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                                                                                                                                                  Sequence 10, Application US/09995529

Publication No. US20040091482A9

GENERAL INFORMATION:
APPLICANT: Watkins, Jeffry D.
APPLICANT: Huse, William D.
APPLICANT: Tang, Ying
TITLE OF INVENTION: Humanized Collagen Antibodies and
TITLE OF INVENTION: Humanized Methods
TITLE OF INVENTION: Related Methods
CURRENT APPLICATION NUMBER: US/09/995,529
CURRENT FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 564; DB 3;
Pred. No. 1.1e-46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 56, Application US/10735916A Publication No. US20050084906A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.6%;
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Best Local Similarity 95.5%;
Matches 107; Conservative
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; ORGANISM: Mus musculus
US-09-995-529-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Mus musculus US-10-735-916A-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                       US-09-995-529-10
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                                          APPLICANT: GORNALA, Nathalie
APPLICANT: GORNALA, Nathalie
APPLICANT: DEGER, Olivier
APPLICANT: DUFLOS, Alain
APPLICANT: DUFLOS, Alain
APPLICANT: DUFLOS, Alain
APPLICANT: HAEUW, Jean-Francoie
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REFERENCE: 01753-138
CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT APPLICATION NUMBER: PR 03/08 538
PRIOR APPLICATION NUMBER: PR 03/08 538
PRIOR APPLICATION NUMBER: PR 02/00 653
PRIOR PILING DATE: 2003-01-10
PRIOR APPLICATION NUMBER: FR 02/00 654
PRIOR APPLICATION NUMBER: FR 02/00 654
PRIOR APPLICATION NUMBER: FR 02/05 5753
PRIOR APPLICATION NUMBER: FR 02/05 5753
PRIOR APPLICATION NUMBER: PR 02/05 5753
PRIOR APPLICATION NUMBER: PR 02/05 5753
PRIOR APPLICATION NUMBER: PR 02/05 753
PRIOR A
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Pred. No. 1.1e-46;
1; Mismatches 4; Indels
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| Sequence 10, Application US/09995529
| Publication No. US20030099655A1
| GENERAL INFORMATION:
| APPLICANT: Watkins, Jeffry D.
| APPLICANT: Huse, William D.
| APPLICANT: Tang, Ying
| TITLE OF INVENTION: Related Methods
| TITLE OF INVENTION: Related Methods
| CURRENT APPLICATION WUMBER: US/09/995,529
| CURRENT FILING DATE: 2001-11-26
| NUMBER OF SEQ ID NOS: 358
| SOFTWARE FEASTSEQ for Windows Version 4.0
| SEQ ID NO 10
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Best Local Similarity 100.0%; Pred. No. 3.7e-49;
Matches 112; Conservative 0; Mismatches 0;
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Best Local Similarity 95.5%;
Matches 107; Conservative
                                   APPLICANT: GOETSCH, Liliane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CORGANISM: Mus musculus
US-10-735-916A-49
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US-09-995-529-10
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Sequence 2, Application US/09990205
; Sequence 2, Application US/09990205
; Sequence 2, Application US/09990205
; Patent No. US20020150572A1
; GENERAL INFORMATION:
    APPLICANT: CHATTERJEE, Malaya
    TILLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF PSORIASIS
; FILE REFERENCE: 304142000501
; CURRENT APPLICATION NUMBER: US. 09/192,838
; PRIOR FILING DATE: 1998-11-16
; PRIOR PLILING DATE: 1998-11-16
; PRIOR PLILING DATE: 1998-11-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NOS: 5
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US-10-153-401-66
US-10-153-401-66
Sequence 66, Application US/10153401
Sequence 66, Application US/10153401
GENERAL INFORMATION:
Chatterjee, Malaya
Con, Kenneth A.
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TREATMENT OF MELANOWA AND SMALL CELL CARCINOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DVIATQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL 60
                       1 DVIMIQTPLSLPVSLGDQASASCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIXKVSNRF 60
DVIATQI PLSLPVSLGDQASI SCRSSQSI VHSNGNTVLQAYLQKPGQSPKLLI VKVSNRL
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                                                                                                        61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGIYYCFQGSHVPWTFGGGTKLEI
                                                                                61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEI
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93.4%; Score 551; DB 3; Length 149;
Best Local Similarity 93.8%; Pred. No. 2.7e-45;
Matches 105; Conservative 1; Mismatches 6; Indels
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COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/153,401
FILING DATE: 27-Aug-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Mus Musculus
US-09-990-205-2
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Sequence 4, Application US/10258728

Publication No. US20040091485A1

GENERAL INFORMATION:

APPLICANT: Ellis, John Robert Maxwell

APPLICANT: Ellis, John Robert Maxwell

TITLE OF INVENTION: Humanised Antibodies to the Epidermal Growth Factor Receptor

FILE REFERENCE: 28438-1010S01

CURRENT FILING DATE: 2003-06-18

PRIOR APPLICATION NUMBER: GB 0011981.8

PRIOR APPLICATION NUMBER: GB 0011981.8

PRIOR APPLICATION NUMBER: GB 0020794.4

PRIOR FILING DATE: 2000-08-24

NUMBER OF SEQ ID NOS: 28

SOFTWARE: PatentIn version 3.1

SEQ ID NO 4

LENGTH: 112
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                          1 DVIANTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL 60
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CRGANISM: Mus musculus
US-10-258-728-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Mus musculus
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL 60
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Sequence 10, Application Wolfout School Sequence 10, Publication No. US20040005550A1

GENERAL INFORMATION:
APPLICANT: Shattil, Sanford J.
APPLICANT: Hato, Taka
APPLICANT: Hato, Taka
APPLICANT: Stupack, Dwayne
APPLICANT: Stupack, Dwayne
TITLE OF INVENTION: AFTHODS AND COMPOSITIONS USEFUL FOR TARGETING
TITLE OF INVENTION: ACTIVATED VITRONECTIN RECEPTOR ALPHA V BETA 3
FILE REPERBNCE: NOV0149S
CURRENT APPLICATION NUMBER: US/10/454,660
CURRENT FILING DATE: 2003-06-03
PRIOR APPLICATION NUMBER: PRIOR APPLICATOIN NUMBER: US/09/454,925A

PRIOR APPLICATION DATE: 1999-12-03

PRIOR APPLICATION NUMBER: PRIOR APPLICATOIN NUMBER: US/09/454,925A
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US-10-454-660-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCPQGSHVPWTFGGGTKLEIK 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.4%; Score 551; DB 4; Length 263; 93.8%; Pred. No. 5e-45; tive 1; Mismatches 6; Indels
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                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Catherine M. Polizzi
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 304142000202
                        FILING DATE: 1999-04-15
APPLICATION NUMBER: US 08/372,676
FILING DATE: 1995-01-17
                                                                                                     APPLICATION NUMBER: US 08/591,196
FILING DATE: 1996-01-16
APPLICATION NUMBER: US 09/293,533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 66:
                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 263 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                TELEX: 706141
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 93.8
Matches 105; Conservative
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LENGTH: 219
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61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112

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                                                                                                                                                                                                                                            FOOD, Kenneth A.
Chatterjee, Sunil K.
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
NUMBER OF SEQUENCES: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/153,401
FILING DATE: 27-Aug-2002
CLASSIFICATION NUMBER: US 09/293,533
FILING DATE: 1999-04-15
APPLICATION NUMBER: US 08/372,676
FILING DATE: 1995-01-17
APPLICATION NUMBER: US 08/591,196
FILING DATE: 1995-01-17
APPLICATION NUMBER: US 08/591,196
FILING DATE: 1995-01-16
ATTORNEY/AGENT INFORMATION:
NAME: Cacherine M. Polizzi
REGISTRATION NUMBER: 40,100,000,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 548; DB 4; Length 112;
Pred. No. 3.8e-45;
1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 304142000202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
US-10-735-916A-57
Sequence 57, Application US/10735916A
; Publication No. US20050084906A1
                                                                                                                                                  Sequence 15, Application US/10153401; Publication No. US20030114398A1; GENERAL INFORMATION:
                                                                                                                                                                                                                             APPLICANT: Chatterjee, Malaya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 494-0792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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Best Local Similarity
Matches 105; Conserv
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US-10-153-401-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
          GENERAL INFORMATION:

APPLICANT: GORTSCH, Liliane
APPLICANT: GORTSCH, Liliane
APPLICANT: CORVALA, Nathalie
APPLICANT: LEGER, Olivier
APPLICANT: DUFLOS, Alain
APPLICANT: DUFLOS, Alain
APPLICANT: HAEUW, Jean-Francois
ITILE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-183
CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT APPLICATION NUMBER: PR 03/08 538
PRIOR APPLICATION NUMBER: PR 03/08 653
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-01-20
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-05-07
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PATENTIN VET. 2.1

LENGTH: 112

LENGTH: 112

LENGTH: 112
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Publication No. US20040265307A1

GENERAL INFORMATION:

TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
FILE REFERENCE: A669

CURRENT FILING DATE: 2003-12-08

PRIOR PFLICATION NUMBER: 10/170,390

PRIOR FILING DATE: 2002-06-14

NUMBER OF SEQ ID NOS: 96

SOFTWARE: PatentIn version 3.2

LENGTH: 113

TYPE: PRI

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92.7%; Score 547; DB 5;
Best Local Similarity 92.0%; Pred. No. 4.8e-45;
Matches 103; Conservative 5; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: synthetic antibody structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (28)...(28)
OTHER INFORMATION: "X" may be any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: MISC FEATURE
LOCATION: (101)..(101)
OTHER INFORMATION: "X" may be any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Mus musculus
US-10-735-916A-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-729-441-69
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92.7%; Score 547; DB 5; Length 113;

Query Match

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Publication No. US20030114398A1
GENERAL INFORMATION:
APPLICANT: Chatterjee, Malaya
Foon, Kenneth A.
Chatterjee, Sunil K.
TITLE OF INVENTION: TREATMENT OF MELANOMA AND USE FOR THE
TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL
                                                                          1 DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL
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                        0; Gaps
                                                                                                                                                                            61 YGVPDRPSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
                                                                                                                                                                                                             61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCPQGSHVPXTFGGGTKLEIK 112
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                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ImmunoGen, Inc.
TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
FILER REFERENCE: A8338
CURRENT APPLICATION NUMBER: US/10/897,406
CURRENT FILING DATE: 2004-07-23
PRIOR APPLICATION NUMBER: US/10/170,390
PRIOR PILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin version 3.1
SEQ ID NO 69
ilarity 93.8%; Pred. No. 4.8e-45;
Conservative 1; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atch
cal Similarity 93.8%; Pred. No. 4.8e-45;
105; Conservative 1; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: synthetic antibody structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: MISC FEATURE LOCATION: (28). (28) OTHER INFORMATION: "X" may be any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: MISC FRATURE
1 LOCATION: (101)...(101)
2 OTHER INFORMATION: "X" may be any amino acid
US-10-897-406-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESSE
ADDRESSES:
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                  Sequence 69, Application US/10897406; Publication No. US20050186203A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 105; Conserv
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: PLOPPY disk

MEDIUM TYPE: Floppy disk

COMPUTER: IM PC COMPATA:

OCHAPITATION SUPPLY: PCD05/MS-D05

SOFTWARE: PARENIEN Release #1.0, Version #1.30

DEFLICATION NUMBER: US/00/153,401

FILING DATE: 1995-04-15

APPLICATION NUMBER: US 09/293,533

FILING DATE: 1995-04-15

APPLICATION NUMBER: US 09/291,533

FILING DATE: 1995-04-15

APPLICATION NUMBER: US 09/291,196

APPLICATION NUMBER: US 08/372,676

FILING DATE: 1995-04-15

APPLICATION NUMBER: US 09/291,196

APPLICATION NUMBER: US 00/291,196

APPLICATION NUMBER: US
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Search completed: January 10, 2006, 21:35:30 Job time : 62.4328 secs

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January 10, 2006, 20:07:41; Search time 77.3134 Seconds (without alignments) 636.505 Million cell updates/sec
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590
1 DVLMTQIPLSLPVSLGDQAS......CRQGSHVPWTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                  2443163
GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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Maximum Match 100%
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Adj76888 Anti-IGF-		Adj76883 Anti-IGF-		Add94125 Mouse HUI	Adj76890 Anti-IGF-	Adz67060 Mouse ant	Aae15704 Mouse mon	Aeb21358 Mouse ant		Adi26498 Human ECL		Adp84941 Variable		Ads88785 Sequence			Aaw03199 Anti-idio	Aay21545 Monoclona	0	Ada14828 Anti-idio	Monocl	Amino	Aap81364 Light cha
SUMMARIES		a	ADJ76888	ADZ67058	ADJ76883	ADZ67053	ADD94125	ADJ76890	ADZ67060	AAE15704	AEB21358	AEB31116	AD126498	AD126490	ADP84941	AEC21825	ADS88785	ADP84942	AAP80154	AAW03199	AAY21545	AAY28470	ADA14828	ADC35357	ADS88781	AAP81364
		8	7	σ	7	σ	7	7	6	Ŋ	σ	0	æ	œ	æ	σ	œ	œ	-	~	~	~	9	7	8	-
		Length	112	112	122	122	112	112	112	112	114	114	114	114	114	139	238	114	249	149		263		263	113	115
d	Query	Match	100.0	100.0	100.0	100.0	92.6	92.6	92.6	94.6	94.6	94.6	94.2	94.1	94.1	94.1	94.1	93.7	93.6	93.4	93.4	93.4	93.4	93.4	93.2	93.2
		Score	590	590	590	590	564	564	564	558	558	558	556	555	555	555	555	553	552	551	551	551	551	551	550	550
	Result	NO.	п	~	٣	4	'n	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24

	Abp52310 Fv region Aay49217 Light cha Ada14777 Peptide f Adc35319 Anti-idio				Adp84958 Single ch Adp84957 Single ch Adp84956 Single ch Adp84955 Single ch Adp84954 Single ch
1 AAB62301 3 AAY95258 3 ADS88777	5 ABP52310 2 AAY49217 5 ADA14777 7 ADC35319	3 ADP84938 3 ADP84966 3 ADP84971	3 ADP84964 3 ADP84963 3 ADP84962	3 ADP84961 3 ADP84960 3 ADP84959	3 ADP84958 3 ADP84957 3 ADP84956 3 ADP84955 3 ADP84954
115 219 298	21112	219	257 E 258 E 259 E	260 261 262 8	264 264 265 265 265
					888892.9 92.9 92.9
	54 45 54 48 54 88 44 54 88 84	0 0 0	24 C C C	0. 0. 0.	5 4 4 8 8 8 4 8 8 8 8 8 8 8 8 8 8 8 8 8
25 26 27	3 2 2 6	3 3 3 4	35	398	4444

## ALIGNMENTS

8884 400	RESULT 1 ADJ76888 Standard; protein; 112 AA. XX ADJ76888; XX ADJ76888; XX ADJ76888; XX Anti-1GF-1R related protein #5. XX O-MAY-2004 (first entry) XX O-MAY-2004 (first entry) XX Anti-1GF-1R related protein #5. XX XX Anti-1GF-1R related protein #5. XX	
88888888	The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and its franchicator receptor (EGFR) and/or with	
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            transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate. Jung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-1R and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; darmatological disease; immune disorder; immunoglobulin; light chain variable region.
                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunoglobulin light chain variable region 7C10 VL SEQ ID NO:54.
                                                                                                                                                                                                       DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL
                                                                                                                                                                                                                                  DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL
                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
                                                                                                                                                                                                                                                                  61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beck A;
                                                                                                                                               Length 112;
 these receptors with their ligands. Especially they inhibit
                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haeuw J,
                                                                                                                                                                             ö
                                                                                                                                             Score 590; DB 7;
Pred. No. 1.2e-45;
                                                                                                                               100.0%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Duflos A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 12; SEQ ID NO 54; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                     ADZ67058 standard; protein; 112 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leger O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; 2002FR-0000653.
; 2002FR-0000654.
; 2002FR-00065753.
; 2003WO-FR000178.
; 2003FR-00008538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-DEC-2003; 2003US-00735916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                            Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goetsch L, Corvaia N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2005-321968/33
                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GOETSCH L.
CORVAIA N.
LEGER O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DUFLOS A. HAEUW J.
                                                                                                                   Sequence 112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2005084906-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BECK A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JAN-2002;
07-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-JUL-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-JAN-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-APR-2005.
                                                                                                                                                                                                                                                                                                                                                                                               ADZ67058;
                                                                                                                                               Query Match
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(LEGE/)
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(HAEU/)
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Treeperor (IGF-IR) antibody (I) or its functional fragment, being capable of spable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting trowner kinase activity of the receptor.

Comprishing a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (AD267006 and AD267014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or connected with an overexpression and/or an abnormal contractivation of the transduction pathway of the signal mediated by the interaction of the IGF-IR and/or EGFR, and/or connected with a medicament does not induce or only slightly interaction of the transformation of normal cells into cells with tumoral contractor. The antibody is useful for preparation of a medicament intended to inhibit the growth or induce secondary effects connected with inhibition of the insulin capacitary preferably IGF-dependent, especially IGF-dependent and/or EGF-dependent and/or HERZ/neu-dependent and/or EGF-dependent and/or HERZ/neu-dependent of a medicament intended for prevention or for the treatment of cancer, where the cancer is chosen from proparation of a medicament intended for prevention or for the treatment of amedicament intended for prevention or for the treatment of section of a medicament intended for prevention or for the treatment of postals in the preparation of a medicament intended for prevention or for the prevention or for the cancer, where the cancer, endometrial cancer or colon cancer. (I) is useful in the preparation of a medicament intended for the specific targeting of a biological septended by an overexpression or an underexpression of the IGF-IR and/or EGFR receptor. (I) is useful for in vitro diagnosis of illnesses induced by an overexpression or an underexpression of the IGF-IR and/or EGFR receptor. It is use
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invention relates to a novel isolated anti-insulin-like growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DVLMTOIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGOSPKLLIYKVSNRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 590; DB 9; 100.0%; Pred. No. 1.2e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytostatic; antipsoriatic; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADJ76883 standard; protein; 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-IGF-1R related protein #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2003059951-A2.
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셤
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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or retar diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Bapecially they inhibit transformation of normal cells, so are useful against cancers of the prostate, lung, breast, endomerrium and colon, also osteosarcoma, and also for treating psoriasis, Ab are a also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein sequence used to generate the Ab of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 49; 164pp; French
                                                                                                                                                                                                                                                               (FABR ) FABRE MEDICAMENT SA PIERRE
                                                                                                                                                                                                                                                                                                                                                         Leger O;
20-JAN-2003; 2003WO-FR000178
                                                                                18-JAN-2002; 2002FR-00000653.
18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
                                                                                                                                                                                                                                                                                                                                                         Corvaia N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-569653/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 122 AA;
                                                                                                                                                                                                                                                                                                                                                         Goetsch L,
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Gaps ö 100.0%; Score 590; DB 7; Length 122; 100.0%; Pred. No. 1.3e-45; tive 0; Mismatches 0; Indels 0 Matches 112; Conservative Local Similarity Query Match #X###X#X#X#X#X##X

9 70 DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL н 11 셤 ઠ

YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCPQGSHVPWTFGGGTKLEIK 112 61

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ADZ67053 standard; protein; 122 AA 30-JUN-2005 ADZ67053 THE LEFT SON THE STATE OF THE S

(first entry)

immunoglobulin light chain variable region 7C10 VL SEQ ID NO:49.

Murine

Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; immunoglobulin; light chain variable region.

Mus musculus.

1. .10 /note= "leader peptide" Location/Qualifiers /note= "CDR1" .49 Peptide Region

Corvaia N, Leger O, Duflos A, Haeuw J, 65. .71 /note= "CDR2" 104. .111 /note= "CDR3" 18-JAN-2002; 2002FR-0000654. 07-MAY-2002; 2002FR-00005753. 20-JAN-2003; 2003WO-FR000178. 11-JUL-2003; 2003FR-00008538. 16-DEC-2003; 2003US-00735916 2002FR-00000653 WPI; 2005-321968/33. GOETSCH L. CORVAIA N. LEGER O. DUFLOS A. HAEUW J. N-PSDB; ADZ67052 US2005084906-A1 BECK A. 18-JAN-2002; 21-APR-2005 Goetsch L, (DUFL/) (HAEU/) (BECK/) (GOET/) CORV/ Region Region (LEGE/

Ä Beck Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) artibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer. Example 8; SEQ ID NO 49; 125pp; English.

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The invention relates to a novel isolated anti-insulin-like growth factor.

Treceptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tyrosine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary comprising a light or heavy chain having at least one complementary comprising a light or heavy chain having at least one complementary caids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of a milneas connected with a noverexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or of EGFR, and/or EGFR, and and/or EGFR, and/or EGFR, and and/or EGFR, an overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (1), which is optionally labeled. The present sequence is used in the exemplification of the invention.

122 AA; Sequence ö

Gaps

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4; Indels

Mismatches

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107; Conservative

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fragment comprising one or more complementarity determining regions cides of a defined light CDR and a heavy CDR with at least one amino acid (as) substitution where the antibody has specific binding activity for a cryptic collagen epitope. The growth of all solid tumours requires new blood vessel growth, anglogenesis, inhibition of which is an approach to limiting tumour growth. The invention may allow development of therapeutics with a cytostatic activity as a collagen agonist or antagonist. The invention is useful for diagnosing and treating disorders associated with anglogenesis, tumour growth and/or cancer metastasis. The present sequence is the partial amino acid sequence of the mouse anticryptic collagen site antibody HII77 variable region light chain used during the creation of the antibody of the invention.
                                                              9
                                                                                     20
                                                                           DVLATQI PLSLPVSLGDQASI SCRSSQSIVHSNGNTYLQWYLQKPQQSPKLLIYKVSNRL
                                                             DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL
                                                                                                                                                                                                                                                                                              grafted antibody, complementarity determining region, CDR; light CDR; heavy CDR; cryptic collagen epitope; solid tumour; new blood vessel growth; anglogeneeis; tumour growth; cytostatic; collagen agonist; cancer metastasis; anti-cryptic collagen; antibody; HUI77; variable region light chain; mouse; murine.
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention relates to a novel grafted antibody or its functional
                                                                                                                                                                                                                                                                        Mouse HUI77 variable region light chain partial amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New cryptic collagen antibody with one or more complementarity determining regions, useful for diagnosing and treating disorders associated with angiogenesis, tumor growth and/or cancer metastasis.
                                                                                                           61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
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              Length 122;
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                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Broek D, Brooks PC;
            Score 590; DB 9;
Pred. No. 1.3e-45;
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Pred. No. 2.6e-43;
100.0%; Scor.
100.0%; Pred. No. 1...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; SEQ ID NO 10; 232pp; English
                                                                                                                                                                                                  ADD94125 standard; protein; 112 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-NOV-2002; 2002WO-US038147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-NOV-2001; 2001US-00995529.
06-DEC-2001; 2001US-00011250.
                                                                                                                                                                                                                                                 (first entry)
                                     Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CELL-) CELL MATRIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Huse WD,
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N-PSDB; ADD94124.
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Best Local Similarity
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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or creat diseases associated with overexpression and/or abnormal activity of IGF-IR. Ab and its fragments are used to prevent or IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic; antipsoriatic; antibody; insuliarlike growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; BGFR; signal transduction pathway; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                         DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL
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Pred. No. 2.6e-43;
1; Mismatches 4; Indels
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18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-00005753.
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Best Local Similarity 95.5%;
Matches 107; Conservative 1
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Best Local (
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ID ADJ7
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The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGP-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tyrosine kinase activity of the receptor. Comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An autibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGP-IR and/or EGFR, and/or connected with a ctivation of the transduction pathway of the signal mediated by the interaction of IGFI or IGF2 with IGF-IR and/or of EGF with EGFR, where the administration of the medicament does not induces or only slightly induces secondary effects connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended
                                                                                                                                                                                                                                                                                                                 Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; light chain variable region.
antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)
                                                      61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCPQGSHVPWTFGGGTKLEIK 112
                                                                          SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
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                                                                                                                                                                              ADZ67060 standard; protein; 112 AA
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2002FR-0000654.
2002FR-0005753.
2003WO-FR000178.
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CORVAIA N.
LEGER O.
DUFLOS A.
HAEUW J.
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18-JAN-2002;
07-MAY-2002;
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(BECK/)
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cc to inhibit the transformation of normal cells into cells with tumoral character, preferably IGF-dependent, especially IGF1 and/or IGF2-
C dependent and/or EGF-dependent and/or HER2/new-dependent calls. (I) is useful for preparation of tumor cells, preferably IGF-dependent and/or the probliferation of tumor cells, preferably IGF-dependent, and/or LER2/new-dependent and/or EGF-dependent and/or HER2/new-dependent cells. (I) is useful in the preparation of a medicament intended for prevention or for the treatment of cancer, where the cancer is chosen from prostate cancer, osteosarcoma, lung cancer, the cancer is chosen from prostate cancer, osteosarcoma, lung cancer, or preparation of a medicament intended for the prevention or for the prevention of a medicament cancer or colon cancer. (I) is useful in preparation of a medicament cancer or colon cancer. (I) is useful in preparation of a medicament cancer or colon cancer. (I) is useful in preparation of a medicament cancer or colon cancer. (I) is useful for in vitro diagnosis of a biologically active compound to cells expression or an underexpression of the IGF-IR and/or EGFR receptor is useful for in vitro diagnosis of illnesses induced by an overexpression or an underexpression of the IGF-IR and/or EGFR receptor is usepected, which involves contacting the biological sample with (I), which is optionally labeled. The present contacting the cancer is used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse; humanised form; monoclonal antibody alpha 340; gene therapy; epidermal growth factor receptor; EGF; cancer; colorectal; lung; breast gastric; ovarian; immune response; cytostatic; cell growth; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DVLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 564; DB 9; Length 112;
Pred. No. 2.6e-43;
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24-AUG-2000; 2000GB-00020794.
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|abel= CDR1
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/label= CDR2
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/label= CI
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                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 112 AA;
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inhibitor.
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(TANO-) TANOX INC.

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The present invention relates to a humanised form of the antibody 340 (a mouse monoclonal antibody which binds to epidermal growth factor (EGF) receptor and inhibits binding of EGF), obtainable from the cell line deposited with the ECACC under accession number 97021428. The humanised form of the antibody 340 is useful in gene therapy, medicine and in the manufacture of a medicament for treatment or prophylaxis of cancer. The manufacture of a medicament for treatment or prophylaxis of cancer. The invention is useful for treating colorctal, lung, breast, gastric or ovarian cancers or also for preventing the recurrence of cancer after initial treatment or surgery. The invention is also useful for enhancing a protective immune response against cancer by optimised immunisation schedules. The humanised form of the antibody 340 has reduced immune is the original murine antibody and has increased ability to receptor, as the original murine antibody and has increased ability to receptor, as the original murine antibody and has increased ability to inhibit the growth of EGF receptor expressing cells. The invention is used as cell growth and apoptosis inhibitor. The present sequence is mouse monoclonal antibody alpha 340 light chain variable (VK) region
                                                                                                                                                                                               New humanized form of mouse monoclonal antibody 340 which binds to epidermal growth factor receptor and inhibits binding of growth factor, useful for treating colorectal, lung, breast, gastric and ovarian cancer.
                                                                                                                                                                                                                                                                                                                     Claim 6; Fig 2; 53pp; English.
                                                        Ellis JRM, Durrant LG;
(SCAN-) SCANCELL LTD.
                                                                                                                   WPI; 2002-062384/08.
                                                                                                                                          N-PSDB; AAD25247.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 112 AA;
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9 DVLAMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRF 60 1 DVLATQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL 0; Gaps 61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEI 111 SGVPDRFSGSGSGTDFTLKISRVEAEDLGIYYCFQGSHVPWTFGGGTKLEI 111 Length 112; 4; Indels 94.6%; Score 558; DB 5; 94.6%; Pred. No. 9.1e-43; ive 2; Mismatches 4; Matches 105; Conservative Query Match Best Local Similarity н 셤 δ ઠ

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Interleukin-13; IL-13; antibody engineering; humanized antibody; Antiasthmaticf, Antiaflammatory; Dermatological; Antiallergic; Respiratory-Gen.; Antiulcer, Gastrointestinal-Gen.; Ophthalmological; Osteopathic; Virucide; asthma; allergic rhinitis; atopic dermatitis; Mouse anti-IL-13 antibody 227-26 light chain variable region (VK) allergic conjunctivitis; eczema, urticaria; allergy; chronic obstructive pulmonary disease; ulcerative colitis; respiratory syncytial virus infection; uveitis; scleroderma; osteoporosis; monoclonal antibody; light chain variable region. AEB21358 standard; protein; 114 AA (first entry) 22-SEP-2005 AEB21358; Mus sp. RESULT 9 AEB21358 BX4XBXBXBXEEEEEEEEEEEEEEEEEEEEEEEE

23-DEC-2004; 2004WO-US043501. WO2005062967-A2. 14-JUL-2005

23-DEC-2003; 2003US-0532130P.

The invention relates to an antibody or its antigen-binding fragment that invention relates to an antibody or its antigen-binding fragment that congralizes human interleukin-13 (IL-13), does not bind specifically and with high affinity to glycosylated and non-congrand included are an antibody that binds to the same epitope as the antibody cited above, an antibody comprising antigen binding cathorial antibody, a hybrideda cell line that produces a monoclonal antibody of the antibody, a hybrideda cell line that produces a monoclonal antibody as the form the light and heavy chain variable regions of the novel antibody, a cell comprising the nucleic acid encoding the antibody, a vector comprising the nucleic acid encoding the antibody and a physiologically acceptable composition (comprising the antibody and a physiologically acceptable corrier, diluent, excipient, or stabilizer), a variable light chain region (composition gan amino acid sequence having the nucleic acid encoding the antibody and a physiologically acceptable composition (comprising the farmino acid sequence having the formula: FRIJ-CDRIJ-FRIJ-C New antibody or its antigen-binding fragment that binds specifically and with high affinity to glycosylated and non-glycosylated human interleukin -13 (IL-13), useful for treating IL-13-mediated disorders, such as asthma ä Huang Singh S, Claim 10; SEQ ID NO 7; 129pp; English. mouse anti-IL-13 monoclonal antibody. Yan C, Σ Ξ WPI; 2005-506603/51. Sequence 114 AA; and eczema. SC, Fung 

1 DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL Gaps ; 0 Length 114; 4; Indels Score 558; DB 9; Pred. No. 9.3e-43; 1; Mismatches 4; 94.6%; ilarity 95.5%; Conservative 1 Similarity Best Local Sim<sup>3</sup> Matches 107; Query Match

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This invention describes a novel method for treating a neoppiage comprises administering an anti-IL-13 antibody or its binding fragment that binds administering an anti-IL-13 antibody or its binding fragment that binds administering an anti-IL-13 antibody or its binding fragment that binds gpecifically and with high affinity to both glycosylated and nonglycosylated human IL-13 activity at an approximate molar ratio of 1:2 (MAD:IL-13). The method also describes 1) and neutralizes human IL-13 activity at an approximate molar ratio of 1:2 (MAD:IL-13). The method also describes 1) thumanized or chimeric antibody or binding fragment to a patient; 2) inhibiting IL-13 dependent proliferation of neoplastic cells in a mammal comprising administering the antibody or a binding fragment that inhibits the biological activity of IL-13 and 3) diagnosing a cancer or tumor overexpressing IL-13 comprising the use of the anti-IL-13 antibody conditions are patient suspected of having the cancer or tumor. The antibodies used in the method of the invention are 228B/C produced by the hybridoma designated PTA-5657, 228A-4 and produced by the hybridoma designated PTA-5657, 227-26 produced by the hybridoma designated PTA-5657, or 227-43 produced by the hybridoma designated PTA-5657, or 227-43 conduced by the antibody a single domain antibody or a humanized antibody a single domain antibody or a humanized combinations. The antibody further comprises a physiologically acceptable carrier, diluent, excipient, or stabilizer. The antibody mediates killing the antibody dependent cell-mediated cytotoxicity and vorcer a very partial patient of the patient cell-mediated cytotoxicity and vorcer and pendiates when a least a variable PTA-6000 antibody and produced by antibody and pendiate subtant and produced by antibody and 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDRIJ-FRIZ-CDRIZ-FRIJ-CDRIJ-FRL4. The antibody comprises at least a variable light or heavy chain region. The variable light or heavy chain region further comprises a constant region. The constant region is from an IgG antibody. The IgG antibody is an IgG1, IgG2, IgG3 or an IgG4 antibody. The antibody further comprises the heavy chain. The antibody is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating a neoplasm, e.g. Hodgkin's disease, that expresses and/or binds interleukin-13 (IL-13) comprises administering an anti-IL-13 antibody or its binding fragment that binds to both glycosylated and non-glycosylated
                                                                                                                                                                                                                  cytostatic; antibody therapy; neoplasm; interleukin 13; IL-13; cancer; diagnosis; tumor; humanized antibody; cell proliferation; Hodgkins disease; cytotoxin; chemotherapy; lymphoma; skin tumor; stomach tumor; colon tumor; breast tumor; pancreatic tumor; liver tumor; prostate tumor; lung tumor; head and neck tumor; renal tumor; liver tumor; squamcus cell carcinoma; brain tumor; Raposis carcinoma; solid tumor; monoclonal antibody; 227-26; 227-26-1; light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chain region comprising an amino acid sequence having the formula: FRL1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes a novel method for treating a neoplasm that
                                                                                                                                                                 Antibody 227-26/227-26.1 variable light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 13; SEQ ID NO 7; 98pp; English.
AEB31116 standard; protein; 114 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-DEC-2004; 2004WO-US043541.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-DEC-2003; 2003US-0532130P.
                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TANO-) TANOX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Moyle M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2005062972-A2
                                                                                                          22-SEP-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human IL-13
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus sp.
Synthetic.
                                                      AEB31116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 al antibody enzymes by identification of a catalytic n the stereostructure for production of antibody enzymes therapeutic agents for cancer and infectious diseases
associated with a cytotoxic agent, such as a radioisotope or a chemotherapeutic agent. The methods and antibodies are useful for treating neoplasms such as Hodgkin's lymphoma, skin cancer, stomach cancer, colon cancer, breast cancer, pancreatic cancer, liver cancer, prostate cancer, lung cancer, head-and-neck cancer, renal cell cancer, aguanque sell carrinoma, AIDS-associated Kaposi's carcinoma and brain cancer. This sequence represents the humanized mouse monoclonal antibody 227-26 and 227-26-1 variable light chain.
                                                                                                                                                                                                                                                              DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL 60
                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                    SGVPDRFSGSGSGTDFTLKISRVEABDLGVYYCFQGSHVPYTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                  61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibody; enzyme; virucide; anti-HIV; cytostatic; antibacterial; helicobacter pylori urease inhibitor; chemokine receptor CCR-5 antagonist; cancer; infectious disease;
                                                                                                                                                                                                                              ö
                                                                                                                                                                                      Score 558; DB 9; Length 114;
Pred. No. 9.3e-43;
1; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Screening potential antibody enzymes by tripler residue in the stereostructure as diagnostic and therapeutic agents for including HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADI26498 standard; protein; 114 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicobacter pylori; HIV; human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-JUL-2003; 2003WO-JP009147.
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2003JP-00051943.
2003JP-00198270.
                                                                                                                                                                                          / Match 94.6%;
Local Similarity 95.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2003JP-00198292
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                                                                                                                                                                                                                                Matches 107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ADI26499
                                                                                                                                                           Sequence 114 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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27-FEB-2003;
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                                                                                                                                                                                               Query Match
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residue are located sterically close to one another. An enzyme produced

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        by the method of the invention has virucide, anti-HIV, cytofratic, and antibacterial activity. The enzyme acts as a helicobacter pylori urease inhibitor, or chemokine receptor CCR-5 (HIV target) antagonist. The method of the invention is useful for the treatment, prevention and diagnosis of cancer and infectious diseases, especially infection by Helicobacter pylori or HIV. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                  DVLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKFLIYKVSNRF
                                                                                                                                                                                                  1 DVLATQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL
                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                      61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCPQGSHVPWTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                    SGVPDRFSGSGSGTDFTLKISRVETEDLGVYYCFQGSHVPWTFGGGTKLRIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibody; enzyme; virucide; anti-HIV; cytostatic; antibacterial; helicobacter pylori urease inhibitor; chemokine receptor CCR-5 antagonist; cancer; infectious disease; Helicobacter pylori; HIV; human.
are located sterically close to one another. An enzyme
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0
                                                                                                                                            Length 114;
                                                                                                                                                                        6; Indels
                                                                                                                                             Score 556; DB 8;
Pred. No. 1.4e-42;
                                                                                                                                                                        1; Mismatches
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2003JP-00051943.
2003JP-00198270.
                                                                                                                                           94.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                             Human ECL2B-2-L SEQ ID NO:26.
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17-JUL-2003; 2003JP-00198292.
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                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                        Matches 105; Conservative
                                                                                                                                                           Local Similarity
                                                                                                                   Sequence 114 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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27-FEB-2003;
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Screening potential antibody enzymes by identification of a catalytic triplet residue in the stereostructure for production of antibody enzymes as diagnostic and therapeutic agents for cancer and infectious diseases including HIV infection.

WPI; 2004-132963/13.

N-PSDB; ADI26491

Uda T, Hifumi E;

Claim 39; SEQ ID NO 26; 232pp; Japanese.

The invention relates to a novel method for producing antibody enzymes comprising a structural analysis step which confirms the existence in the predicted stereostructure of the antibody based on its amino acid sequence of a catalytic triplet residue structure in which a serine residue, an aspartic acid residue, and a histidine or glutamic acid

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recognition molecules, e.g. antibodies (and nucleic acids) that bind specifically to Core-1 antigens, useful for diagnosis, treatment and
           by the method of the invention has virucide, anti-HIV, cycostatic, and antibacterial activity. The enzyme acts as a helicobacter pylori urease inhibitor, or chemokine receptor CRR-5 (HIV target) antagonist. The method of the invention is useful for the treatment, prevention and diagnosis of cancer and infectious diseases, especially infection by Helicobacter pylori or HIV. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibody; Core-1 antigen; framework region; immunoglobulin superfamily; protease inhibitor; lectin; helix-bundle protein; lipocalin; variable heavy chain; VI; varcine; diagnosis; alleviation; treatment; tumour; breast; colon; stomach; pancreas; large/small intestine; ovary; cervix; lung; prostate; kidney; liver;
                                                                                                                                                                                                                                                                                                           1 DVLATQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIXKVSNRF
                                                                                                                                                                                                                                                                                       1 DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL
                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                    SGVPDRFSGSGSGTDFTLKINRVAABDLGVYYCFQGSHVPWTFGGGTKLEIK 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Variable light chain VL fragment Karo6 SEQ ID NO 83.
                                                                                                                                                                                                          94.1%; Score 555; DB 8;
93.8%; Pred. No. 1.7e-42;
tive 2; Mismatches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prevention of tumors and metastases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADP84941 standard; protein; 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2003; 2003WO-DE003994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-NOV-2002; 2002DE-01056900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                               Best Local Similarity 93.8
Matches 105; Conservative
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                                                                                                                                                                      Sequence 114 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus.
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                                                                                                                                                                                                            Query Match
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lysine-rich region and/or a multimerisation domain, most particularly it is a single-chain antibody fragment, multibody, Fab fragment, fusion protein of an antibody fragment with peptide or protein, and/or an ig of types G, M, A, E or D and/or their subclasses. It may be human, anditional sequences/structures in the constructs are ig domains of additional sequences/structures in the constructs are ig domains of various species, interacting or stabilising domains, signal sequences, interacting or stabilising domains, signal sequences, tluorescent dyes, toxins, antibodies with catalytic activity or other specificities, cytolytic agents, enzymes, immuno-modulators or effectors, MHC molecules, antigens, chelators for radioactive labels, liposomes, transmembrane domains, viruses and/or cells, specifically, cand encoding them, and related vectors and host cells, are useful for prevention (e,g. as vaccine), diagnosis, alleviation, treatment, concentry pancreas, large/small intestine, overy, cervix, lung, constate, kidney and/or liver) and/or metastases (particularly to liver), specifically where these are positive for the Cl antigen. The products of the invention provide simple, reliable and efficient detection of tumours. They are specific for carcinoma and show almost no binding to healthy tissue.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DVLAMIQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a chimeric antibody specific for human basic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric antibody specific for human basic fibroblast growth factor, useful for preventing and treating pneumosilicosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse light chain variable region amino acid sequence SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCPQGSHVPWTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPYTFGGGTKLEIX 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 114;
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Pred. No. 1.7e-42;
2; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AEC21825 standard; protein; 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.1%;
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Matches 106; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2005-296785/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYJI-) UNIV JINAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AEC21824
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 114 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-OCT-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CN1560082-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JAN-2005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xiang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AEC21825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Мив вр.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AEC2182
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                                                                                                                                                                                                                                                       20 DVLMTÓTPLSLPVSLGDÓASÍSCRSSÓSÍVHSNGNTYLEWYLOKPGÓSPKLLIYKVSNRF 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antibody against the G glycoprotein of RSV with a variable region having a first and second domain from a VL and VH region, respectively, useful for treating respiratory syncytial virus (RSV) infections.
                      σĘ
                                                                                                                                                                                                                      DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G glycoprotein, respiratory syncytial virus;
respiratory syncytial virus infection; RSV; RSV infection; IC2; IgG1;
                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence of the chimeric IC2 kappa light chain in M13mp19 clone M609
fibroblast growth factor (bFGF) and its encoding gene. The chimeric antibody contains mouse variable regions and human constant regions human igglc. The antibody is useful for preventing and treating pneumosilicosis. The present sequence represents a mouse light chain variable region which can be used in a chimeric antibody of the
                                                                                                                                                                                                                                                                                        61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                           80 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCPQGSHVPYTFGGGTKLEIK 131
                                                                                                                                                                                       ö
                                                                                                                                                    Length 139;
                                                                                                                                                  Score 555; DB 9; Length 13 Pred. No. 2.2e-42; 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .19
/note= "Ig leader sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mekseepralard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; SEQ ID NO 55; 93pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                             ADS88785 standard; protein; 238 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYNE-) UNIV NEWCASTLE-UPON-TYNE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-MAR-2004; 2004WO-GB001239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-MAR-2003; 2003GB-00006618
                                                                                                                                                      94.18;
                                                                                                                                                                     Local Similarity 94.6%;
nes 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Routledge E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-691033/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ADS88784
                                                                                                                       Sequence 139 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2004083373-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus sp.
Homo sapiens.
Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-SEP-2004.
                                                                                        invention
                                                                                                                                                                                                                        н
                                                                                                                                                                                                                                                                                                                                                                                                                                            ADS88785;
                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Toms G,
                                                                                                                                                                           Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
ADS88785
      8888888
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CC clone carries a mouse-human IgG1 chimeric antibody comprising IC2
CC variable regions and human kappa light chain and gammal heavy chain
CC constant regions.
XX
SQ Sequence 238 AA;
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	· 0	09	79
	0; Gaps	KVSNRL	KVSNRF
	ö	LLIY	
94.1%; Score 555; DB 8; Length 238; 92.9%; Pred. No. 3.8e-42;	; Indels	1 DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL 60	20 DVLMTQTPLSLPVSLGDQASISCRSSQNIVHSDGNTYLEWYLQKPGQSPKLLIYKVSNRF 79
Similarity	at	DVLMTQIPLSLPVSLGDQ	DVLMTQTPLSLPVSLGDQ?
Query Match Best Local	Matches 10	9,	Db 20

Search completed: January 10, 2006, 20:44:13 Job time: 79.3134 secs

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GenCore version 5.1.6 (c) 1993 - 2006 Compugen Ltd.
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January 10, 2006, 20:28:02; Search time 13.5124 Seconds (without alignments) 797.508 Million cell updates/sec Run on:

Title: Perfect score:

US-10-735-916A-54 590 1 DVLMTQIPLSLPVSLGDQAS......CFQGSHVPWTFGGGTKLEIK 112 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		d			SUMMAKIES	
Result No.	Score	Query Match	Length	DB	αI	Description
-	549	93.1		7	B39276	lig
7	547	92.7	112	~	A31807	kappa chain
٣	547	92.7		~	PC4203	
4	546	92.5		~	S26335	kappa chain
2	542	91.9		N	PL0203	i -DNA
9	540	91.5	219	N	S52028	
7	536	90.8		N	PT0359	kappa
œ	536	8.06		~	B34904	kappa chain
σ	535	90.7		N	F27887	kappa chain
10	535	90.7	114	~	A32967	kappa
11	534	90.5		~	B31485	kappa chain
12	533	90.3		~	S38719	light
13	532	90.2		N	C34904	kappa chain pr
14	531	90.0	225	~	JL0029	kappa chain
15	530	89.8		~	A27887	kappa chain
16	528	89.5		~	D28195	kappa
17	527	89.3		~	E27887	kappa
18	527	89.3		N	C27887	kappa
19	527	89.3		~	\$16112	kappa chain V
20	526	89.5		~	B32967	kappa
21	526	89.2		Ŋ	B32513	kappa
22	524	88.8	112	~	A49715	kappa chain
23	522	88.5		~	S53750	ibody
24	521	88.3		~	S32189	
25	521	88.3		~	S38715	kappa
26	521	88.3		~	\$09259	kappa
27	519	88.0	11	~	A34353	i-pep
28	518	87.8		~		hain
29	518	87.8	131	~	D34904	kappa

RESULT 2
A31807
Ig kappa chain V region (PACI) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 20-Jul-1989 #sequence\_revision 20-Jul-1989 #text\_change 09-Jul-2004
C;Date: 20-Jul-1989 #sequence\_revision 20-Jul-1989 #text\_change 09-Jul-2004
C;Date: 20-Jul-1989 #sequence\_revision 20-Jul-1989 #text\_change 09-Jul-2004
C;Date: 20-Jul-1989 #sequence\_revision 264, 259-265, 1989
A;Title: A monoclohal antibody against the platelet fibrinogen receptor contains a sequally fine preliminary
A;Reference number: A31807
A;Accession: A31807
A;Accession: A31807
A;Accession: Pacliminary
A;Molecule type: mRNA
A;Residues: 1-112 c7AU>
A;Coss-references: UNIPARC:UPI00001424F9
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotecramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <INM>

92.7%; Score 547; DB 2; Length 112;

Query Match

Ig kappa chain pre	Ig kappa chain pre	Ig kappa chain V r	kappe	Ig light chain V r	$_{ m 1ight}$	kappe	kappa	kappa	kappa	i-dic	Ig kappa chain V r		Ig kappa chain pre	Ig light chain V r	Ig kappa chain V r
D29380	2 B30577	B27887	PL0257	PH1043	: B41940	S52449	360066	L KVMS26	2 G34903	PH0106	2 E32530	2 S67944	2 PT0178	PH1042	S15673
131 2	131 2	112 2	111 2	103 2	113 2	131 2	115 2	113 1	131 2	132 2	108 2	121 2	131 2	103 2	111 2
87.8	87.8	87.6	87.5	87.3	87.3	87.1	86.8	86.4	86.4	86.4	86.1	85.9	85.8	85.6	85.4
518	518	517	516	515	515	514	512	210	510	510	508	507	206	505	504
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

	RESULT 1	
	B39276	
	Ig light chain precursor V-D-J region (6-19) - mouse	
	C;Species: Mus musculus (house mouse)	
	C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Jan-2000	ange 21-Jan-2000
	C; Accession: B39276	
	R;Reininger, L.; Berney, T.; Shibata, T.; Spertini, F.; Merino, R.; Izui, S.	ino, R.; Izui, S.
	Proc. Natl. Acad. Sci. U.S.A. 87, 10038-10042, 1990	
	A,Title: Cryoglobulinemia induced by a murine IgG3 rheumatoid factor: skin vasculitis	id factor: skin vasculitis a
	A; Reference number: A39276; MUID:91088540; PMID:2263605	
	A; Accession: B39276	
	A;Status: preliminary	
	A; Molecule type: mRNA	
	A;Residues: 1-131 <rei></rei>	
	A; Cross-references: UNIPARC: UPI0000115153; GB:M55313; NID:g198095; PIDN:AAA63385.1; PID	198095; PIDN:AAA63385.1; PID
	C; Superfamily: immunoglobulin V region; immunoglobulin homology	logy
_	C; Keywords: immunoglobulin	
	F;35-114/Domain: immunoglobulin homology <imm></imm>	
	Query Match 93.1%; Score 549; DB 2; Length 131;	. 131;
	Best Local Similarity 93.8%; Pred. No. 3.3e-43; Matches 105; Conservative 2; Mismatches 5; Indels	ls 0; Gaps 0;
	Qy 1 DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNIYLQMYLQRPGQSPKLLLIXVSNKL 60	GOSFKLLIKVSNRL 60
	Db 20 DVLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRF 79	GOSPKLLIYKVSNRF 79
	Qy 61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112	GTKLEIK 112
	DD 80 SGVPDRFSGSGSGTDFTLKISRVBABDLGVYYCFQGSHVPYTFGSGTKLBIK 131	GINTER 131
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C;Dāte: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000 C;Accession: PL0203 R;Smith, R.G.; Voss Jr., E.W. R%:Immunol. 27, 463-470, 1990 A;Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from N A;Reference number: PL0198; MUID:90309768; PMID:2114528
                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-113 <SMI>
A;Cross-references: UNIPARC:UP10000113786; GB:X53643; NID:g50196; PIDN:CAA37694.1; PID:
ED:

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ig kappa chain - mouse
Cispecies: Mus musculus (house mouse)
Cjate: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
CjAccession: 552028
Rivan Engelen, F.; Schouten, A.; Molthoff, J.W.; Roosien, J.; Dirkse, W.G.; Schots, A.;
Rivan Engelen, F.; Schouten, A.; Molthoff, J.W.; Roosien, J.; Dirkse, W.G.; Schots, A.;
A; Nebacription: Coordinate expression of antibody subunit genes yields high levels of fur
A; Reference number: S52028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPARC:UP10000114B22; EMBD:L35138; NID:g522336; PIDN:AAA67525.1; PJ C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;16-95/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        anti-DNA autoantibody BV17-31, kappa chain V region - mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DVVMTQTPLSLPVSLGDQASISCRSSQSIVASNGNTYLEWYLQKPGQSPKLLIYKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVLMTQ1PLSLPVSLGDQAS1SCRSSQS1VHSNGNTYLQWYLQKPGQSPKLL1YKVSNRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGVPDKFSGSGSGTDFTLKISRVEAEDLGVYYCPQGSHVPFTFGSGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
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SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPYTFGGGTKLE 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-95/Domain: immunoglobulin homology <1MM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 540; DB 2; Length 21
Pred. No. 3.8e-42;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 542; DB 2;
Pred. No. 1.2e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig kappa chain V region (R4A.12) - mouse (fragment)
C;Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;94-102/Region: complementarity-determining 3 F;101-113/Region: D region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;24-39/Region: complementarity-determining 1 F;55-61/Region: complementarity-determining 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.5%;
92.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-219 <VAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S52028
                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: PL0203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Sim
Matches 103;
   19
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000
C;Date: 31-Dec-1996 #sequence_revision B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.
Gene 173, 257-259, 1996
A;Title: Cloning and characterization of CDNAs coding for heavy and light chains of a mc
A;Reference number: PG4203
A;Reference number: PG4203
A;Residues: 1-219 < kWA>
A;Residues: 1-219 < kWA>
A;Residues: 1-219 < kWA>
A;Residues: 1-219 < kWA>
A;Cross-references: UNIPARC:UPI0001157E4; GB:U29147; NID:g1594225; PIDN:AAC52821.1; PIIC
C;Comment: This protein is specific for human plasma apolipoprotein A-I of high-density
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;1-112/Domain: C region #status predicted <CRG>
F;113-219/Domain: C region #status predicted <CRG>
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Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cipate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
Cipate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
Cipate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
Cipates 226335
Afritie: Antibodies that are specific for a single amino acid interchange in a protein (A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Recession: S26335
A;Residues: 1-110 <STA>
A;Residues: 1-110 <STA>
A;Residues: 1-110 <STA>
A;Residues: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>
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C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
                                                                                           DVLMTO1PLSLPVSLGDQAS1SCRSSQS1VHSNGNTYLQWYLQKPGQSPKLL1YKVSNRL
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                                                                                                                                                                                                                                                61 SGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGSHVPYTFGGGTKLEIK 112
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                               Indels
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Pred. No. 8.7e-43;
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Best Local Similarity 94.5%; Pred. No. 5.2e-43;
Matches 104; Conservative 2; Mismatches 4;
                                  4;
Pred. No. 4.3e-43;
                               4; Mismatches
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92.98;
                               Matches 104; Conservative
Best Local Similarity
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90.5%; Score 534; DB
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                                                                                                                                                                                                                                                                 Best Local Similarity
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C;Species: Mus musculus (house mouse)
C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jul-2000
C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jul-2000
C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jul-2000
C;Date: 27-Jul-1990
B;Bedczsk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A;Title: Active site structure and antigen binding properties of idiotypically cross-real A;Title: Active site structure and antigen binding properties of idiotypically cross-real A;Title: A24903; MUD:90044387; PMID:2104617
A;Reference number: A34903; MUD:90044387; PMID:2104617
A;Residues: preliminary; not compared with conceptual translation
A;Residues: 1-131 < ABD>
A;Cross-references: UNIPARC:UPI0000114FC8; GB:M32384; GB:J05237; GB:J05238; NID:g639656; C;Superfamily: immunoglobulin immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology <IMM>
F;35-114/Domain: immunoglobulin homology <IMM>
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R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

R;Caton, A.J.; Brownlee, G.G.; Staudt, Company of a restricted antibody response to A;Reference number: A91043; MUD:86300658; PMID:2427335

A;Molecule type: DNA

A;Residues: 1-112 <CAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig kappa chain precursor V region (12-40 and 5-14) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jul-2000
C;Accession: B34904; H34904
Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
Accession: PT0359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig kappa chain V region (HIC5-4D1) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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                                              Signefact, R.; Klainer, G.; Turken, A.; Papazian, L.; Diamond, B. J. Exp. Med. 173, 287-266, 1991
A; Filtle: A novel class of anti-DNA antibodies identified in BALB/c h; Reference number: PT0352; MUID:91108325; PMID:1986536
A; Reference number: PT0352; MUID:91108325; PMID:1986536
A; Rocession: PT0359
A; Rolecule 'type: mRNA
A; Residues: 1-118 «SHE>
A; Residues: 1-118 «SHE>
A; Cross-references: UNIPROT:Q8VCI6; UNIPARC:UP10000176AF2
A; Cromment: This protein is an anti-double-stranded DNA antibody.
C; Comment: This protein is an anti-double-stranded DNA antibody.
F;19-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                Score 536; DB 2; Lengtn 11.
Pred. No. 4.5e-42;
7; Indels
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Pred. No. 5.1e-42;
4; Mismatches 7;
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Best Local Similarity 90.2%;
Matches 101; Conservative
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Best Local Similarity 90.2%;
Matches 101; Conservative
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J. Biol. Chem. 264, 1565-1569, 1989
A;Title: Comparison of variable region primary structures within an anti-fluorescein ida
A;Reference number: A31485, MUID:89109167; PMID:2492278
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A;Molecule type: mRNA
A;Cross-references: UNIPROT;Q99M37; UNIPARC:UPI0000176A19
A;Experimental source: strain Balb/c
A;Note: this sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus
C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus
C;Superfamily: immunoglobulin y region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>
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C;Species: Mus musculus (house mouse)
C;Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 09-Jul-2004
C;Accession: B31485
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                                                                                                                                                                                                                                                                                                                     90.7%; Score 535; DB 2; Length 112; 92.0%; Pred. No. 5.3e-42; tive 2; Mismatches 7; Indels
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A, Molecule type: mRNA
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C;Species: Mus musculus (house mouse)
C;Date: 27-Jul-1990 #text_change 09-Jul-2004
C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 09-Jul-2004
C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 09-Jul-2004
C;Accession: C34904; J31-318, J990
A;Tile: Active site structure and antigen binding properties of idiotypically cross-res
A;Reference number: A34903; MUID:90094387; PMID:2104617
A;References: UNIPROT:Q8VCI6; UNIPARC:UPI00001767A8
B;References: UNIPROT:Q8VCI6; UNIPARC:UPI00001767A8
B;Bedayk, M.D.: Johnson, L.S.; Riordan, G.S.; Voss Jr., E.W.
J. Biol. Chem. 264, 1565-1569, 1989
A;Title: Comparison of variable region primary structures within an anti-fluorescein idi
A;Reference number: A31485; MUID:89109167; PMID:2492278
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Rydimanis, A.Y.
Submitted to the EMBL Data Library, November 1993
A;Reference number: S38713
A;Accession: S38719
A;Accession: S38719
A;Accession: S18719
A;Accession: S18719
A;Residues: 1-112 <CIM>A;Residues: 1-12 <CIM>A;Residues: 1-13 <CIM>A;Residues
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A;Molecule type: protein
A;Residues: 20-52 <BE2.
A;Cross-rences: UNIPARC:UP100001767A9
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                          Indels
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89.3%; Pred. No. 6.5e-42;
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Pred. No. 1.2e-41;
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89.3%;
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                                                                          100; Conservative
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A,Title: Point mutations cause the somatic diversification of IgM and IgG2a antiphosphor A,Reference number: JL0029; MUID:88171315; PMID:3127529
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A.Cross-references: UNIPROT.Q99M37; UNIPARC:UPI000017697F
A.Cross-references: UNIPROT.Q99M37; UNIPARC:UPI000017697F
A.Experimental source: strain BALB/c, cell line RP93 hybridoma cell
A.Note: the authors translated the codon CGG for residue 106 as Pro, ACC for residue 135
A.Note: the nucleotide sequence shown is inconsistent with authors' translation because ct except for four positions shown above
C.Comment: The protein is an anti-phosphorylcholine antibody.
C.Reywords: immunoglobulin V region; immunoglobulin homology
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R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
R;Exton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
Smb0 J. S, 1577-1587, 1986
A;Title: Structural and functional implications of a restricted antibody response to a d A;Reference number: A91043; MUID:86300658; PMID:2427335
A;Accession: A27887
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A; Experimental source: strain Balb/c
A; Experimental source: strain Balb/c
A; Note: this sequence was determined from the germline gene
C; Comment: This sequence was isolated from a hybridoma protein that binds influenza virus
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
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C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
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C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
                                                                                                                DVLMTQI PLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYXVSNRL
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R;Chien, N.C.; Pollock, R.R.; Desaymard, C.; Scharff, M.D.
J. Exp. Med. 167, 954-973, 1988
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Broc. Natl. Acad. Sci. U.S.A. 88:8616-8620(1991).

R EMBL; S57999; AAB19971.2; -; mRNA.

R EMBL; S57999; AAB19971.2; -; mRNA.

InterPro; IPR007109; Ig.

R InterPro; IPR007109; Ig.V.

SMART; SMO0409; IG. 2.

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SMART; SMO0406; IG. 2.

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DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Kappa light chain variable region (Fragment).
GN Name=IgG1 anti-TS1 VL;
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                                                                                                                                                                                                                                                                                                                                                                                                              1 DVVMTOTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIXKVSNRR 60
                                                                        NUCLEOTIDE SEQUENCE.
Extandsson A., Holm P., Ullen A., Stigbrand T., Sundstrom B.E.;
"Studies of the interactions between the anticytokeratin 8 monoclonal antibody TS1, its antigen and its anti-idiotypic antibody alphaTS1.", J. Mol. Recognit. 16:157-163(2003).
                                                                                                                                                                                                                                                                                                                                                                                                1 DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL
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     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Novotny J., Margolies M.N.;
Novotny J., Margolies M.N.;
"Amino acid sequence of the light chain variable region from a mouse anti-digoxin hybridoma antibody.";
Biochemistry 22:1153-1158(1983).
-i- MISCELLANEOUS: This chain was isolated from an IgG2a hybridoma protein that binds digoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHV-PWTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQTTHVPPYTFGGGTKLEMK 113
                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                               DB 2; Length 115;
                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                              Erlandsson A.;
Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
EMBL, AJB84575; CAI56337.1; -; mRNA.
InterPro; IPR003599; Ig.
InterPro; IPR00110; Ig-like.
InterPro; IPR003596; Ig.v.
Pfau; PF07686; V-set; 1.
SMART; SM00409; IG; 1.
SMART; SM00409; IG; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                        12560 MW; E4D3BF3D63E88007 CRC64;
                                                                                                                                                                                                                                                                                                                                              86.7%; Score 511.5; DB 2;
87.6%; Pred. No. 8.1e-47;
ive 6; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
RAPPA chain V-II region 26-10.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; Q99M37; 1191.
Ensembl; ENSMUSG0000055315; Mus musculus.
                                                                                                                                                                                                                                                                                                                                                           Local Similarity 87.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                          115
 musculus (Mouse).
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                                                                                                                                                     NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                        115 AA;
                                                  NCBI_TaxID=10090;
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1 DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.; "The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic) antibodies in the GAT system."; EMBO J. 4:3681-3688(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Kappa chain (Fragment).
Mus musculus (Mouse).
Elexaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mus musculus, Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
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InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv. 1.
PROSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Hybridoma; Immunoglobulin domain; Immunoglobulin V region; Monoclonal antibody.
                                                                                                                          Complementarity-determining-1.
                                                                                                                                                                   Complementarity-determining-2.
                                                                                                                                                                                                            Complementarity-determining-3.
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Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                              12273 MW; F9F39CE949A84C2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 AA; 12266 MW; C844B7881A89C18A CRC64;
                                                                                                                                                                                                                                                                                                                                Score 510; DB 1;
Pred. No. 1.1e-46;
5; Mismatches 9;
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83.0%; Pred. No. 1.2e-44;
iive 8; Mismatches 11;
                                                                                                                                                                                                                                                   By similarity.
                                                                                                                                                                                         Framework-3.
                                                                                                                                                Framework-2
                                                                                                       Framework-1
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Q53VP8 MOUSE PRELIMINARY;
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nes 88; Conservative
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Q8TCDO;
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Q8TCD0
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"Cloning and expression of a recombinant mouse Fab-fragment recognizing a defined linear epitope of Chironomus thummi thummi major allergen Chi t I.";
Int. Arch. Allergy Immunol. 110:348-353 (1996).
EMBL, Z37499; CAA85724.1; -; mRNA.
SWR, O65ZC0; 1-219.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                          25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
Kappa light chain C_region (Fragment).
Mus musculus (Mouse).
Bukaryota: Metazoa; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
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Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.
"Human immunoglobulin kappa light chain genes of subgroups II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82.9%; Score 489; DB 2; Length 219; 83.9%; Pred. No. 4.5e-44; ive 7; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Balb/c; TISSUE=Spleen;
MEDLINE=96319505; PubMed=8768802;
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InterPro; IPR003599; IG.
InterPro; IPR003599; IG.
InterPro; IPR003596; IG_C1.
InterPro; IPR003596; IG_C1.
InterPro; IPR003596; IG_V.
Pfam; PP07654; C1-8et; I.
SMART; SM00409; IG; 2.
SMART; SM00407; IGC_I.
PROSITE; PS00359; IG_LIKE; 2.
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STRAIN-Balb/c; TISSUE-Spleen;
                                                      QESZCO MOUSE PRELIMINARY;
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NCBI_TaxID=10090;
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KV2F HUMAN
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z00020; CAA77315.1; -; Genomic_DNA.

BIRS; A01890; KZHURP.

BIRS; A01890; A191.33

BIRS; A01890; BIRS; A191.358; Homo sapiens.

GO; GO:0005956; Cextracellular region; NAS.

GO; GO:0006955; P:immune response; NAS.

InterPro; IPR007110; Ig-like.

InterPro; IPR00710; Ig-like.

BIRS; SS0835; IG_LIKE; 1.

FROSITE; PS50835; IG_LIKE; 1.

FROSITE; PS50835; IG_LIKE; 1.

SIGNAL.

SIGN
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Complementarity-determining-1.
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Complementarity-determining-3.
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SGVPDRFSGSGSGTDFTLKITRVEAEDVGVYFCMQGTHWPSTFGQGTKLEIK 132
                                                                                                                                       (Fragment)
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SEQUENCE
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Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakealey R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
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Klein R., Jaenichen R., Zachau H.G.;
"Expressed human immunoglobulin kappa genes and their hypermutation.";
Eur. J. Immunol. 23:3248-3262(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wagner S.D., Luzzatto L.;
"V kappa gene segments rearranged in chronic lymphocytic leukemia are distributed over a large portion of the V kappa locus and do not show
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                 PubMed=1598223;
Hirabayashi Y., Munakata Y., Sasaki T., Sano H.;
"Variable regions of a human anti-DNA antibody O-81 possessing lupus
nephritis-associated idiotype.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 76.8%; Score 453; DB 2; Length 23 Best Local Similarity 76.8%; Pred. No. 3.7e-40; Matches 86; Conservative 13; Mismatches 13; Indels
                                                                                                                                     TISSUE=Lung;
Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003506; Ig_WHC.
InterPro; IPR003506; Ig_V.
Pfam; PR07654; C1-8et; I.
SMART; SM00406; IGV; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN 1.
Hypothetical protein; Immunoglobulin domain.
SEQUENCE 239 AA; 26235 MW; FACEDC3A3B03871D CRC64;
                                                                                       and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eur. J. Immunol. 23:391-397(1993).
EMBL; BC022362; AAH22362.1; -; mRNA.
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                                                                                                                                                                                                                                                                                                                                        duplicated A regions.";
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PIR; S22658; S22658.
PIR; S34095; S34095.
PIR; S40324; S40324.
PIR; S40374; S40374.
PIR; S42267; S42267.
PIR; S42267; S42267.
HSSP; P01834; 1172.
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NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE.
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PubMed=1601042;
Huber C., Klobeck H.G., Zachau H.G.;
Huber C., Klobeck H.G., Zachau H.G.;
Huber C., Kappa-J kappa a coding joint.";

Eur. J. Immunol. 22:1561-1565 (1992).

EMBL; AR035034; AAD56270.1; -; mRNA.

PIR; 849002; 849002.
                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=1322670;
Stuber F., Lee S.K., Bridges S.L. Jr, Koopman W.J., Schroeder H.W. Jr,
Gaskin F., Fu S.M.;
"A rheumatcid factor from a normal individual encoded by VH2 and V
kappa II gene segments.";
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"V kappa gene segments rearranged in chronic lymphocytic leukemia are
distributed over a large portion of the V kappa locus and do not show
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.5%; Score 451.5; DB 2; Length 114; 77.9%; Pred. No. 2.2e-40; ive 10; Mismatches 14; Indels 1;
                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clin. Immunol. Immunopathol. 87:184-192(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eur. J. Immunol. 23:391-397(1993).
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InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
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Q9UL80_HUMAN PRELIMINARY;
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PIR; S34095; S34095.
HSSP; P01625; 1LVE.
SMR; Q9UL80; 1-114.
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61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112

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Homo sapiens
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Expression driven by an MWTV-LTR enhancer;

Expression Expression B. Engage E. H., Derge J.G.,

Explacted E., Marusina F.S., Wagner L., Schaefer C.F., Bhat N.K.,

Explacton M., Soares M.B., Bonaddo M.F., Casavant T.L., Scheetz T.E.,

Explacton M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Explacton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Explacton M.J., McKernan K.J., Abramson R.D., Mullahy S.J.,

Explacton D.K., Muzny D.M., Sodergren E.J., Lu X., Glabs R.A.,

Explacton E., Ketteman M.J., Madan A., Rodrigues S., Sanchez A.,

Wiltiago M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Explactor D.K., Muzny D.M., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Explactor D.K., Muzny D.M., Schem E.D., Dickson M.C.,

Explactor D.K., Muzny D.M., Green E.D., Dickson M.C.,

Explactical Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,

Explactor D.K., Muzny D.M., Marra M.A.;

Explactor D.K.,
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                                                                                                                                                                                                                                                                                                                                     Mus mušculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWPPWTFGQGTKVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUB=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
Expression driven by an MMTV-LTR enhancer.;
NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 76.1%; Score 449; DB 2; Length 239; Best Local Similarity 76.8%; Pred. No. 9.9e-40; Matches 86; Conservative 9; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MRA-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BC091750; AAH91750.1; -; mRNA.
SMR; O58EU8; 21-239.
GQ; GO:0003823; F:antigen binding; IEA.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.c1.
InterPro; IPR003506; Ig.MC.
InterPro; IPR003596; Ig.W.
InterPro; IPR003596; Ig.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SEQUENCE 239 AA; Z6302 MW; 98FC4BA8EB404215 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                Created)
                                                                                                                                                                                       10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences."
                                                                                                                R MOUSE
QSBEUB_MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF07654; Cl-set; T. SMART; SM0409; IG; 2. SMART; SM0407; IGcl; 1. SMART; SM0406; IGcl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-CZECH II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CZECH II;
                                                                                                                                                                                                                                                                                   lgk-C protein.
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                                                                                  RESULT 9
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MEDLINE-22380257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Magner L., Sheamen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Weßwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Maramed R.D., Mullahy S.J.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVLATQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC063599; AAH63599.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEQUENCE 239 AA; 26245 MW; CD7313DDFFD358B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                239 AA
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PROSITE; PS00290; IG MHC; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; PO1837; IKCU.
SMR; QRP491; 21-237.
InterPro; IPR0031599; IG.
InterPro; IPR003109; IG-11ke.
INTERPO; IRV004109; IG-11ke.
SWART; SW004109; IG-11ke.
                                                                                                                                                                                                                                                                                                               05-JUJ-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 15-JUL-2004 (TrEMBLrel. 27, 14) Pypothetical protein.
                                                                                                                                                                                                                                                QEP491 HUMAN PRELIMINARY;
Q6P491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klauber R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Appkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsich F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rab Stapleton M. J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Brownstein M.J., Wolly D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rab S.A., Walny D.M., Sodergren B.J., Lu X., Gibs R.A.,

Rab Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rad Rabeley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.M., Krzywinski M.I., Skaleka U., Smailus D.E.,

Rad mouse Char A., Schein J.E., Jones S.J.M., Marra M.A.;

Rad mouse Char Analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=1601042;
PubMed=1601042;
Huber C., Klobeck H.G., Zachau H.G.;
Huper C., Klobeck H.G., Zachau H.G.;
"Ongoing V kappa-J kappa recombination after formation of a productive
"Orgoing V kappa coding joint.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Klein R., Jaenichen R., Zachau H.G.;
"Expressed human immunoglobulin kappa genes and their hypermutation.";
Bur. J. Immunol. 23:3248-3262(1993).
EMBI. BC030814; AAH310814.1; -; mRNA.
PIR; S23638; S23638.
PIR; S34091; S34091.
PIR; $40342; $40342.
                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=8436174;
Wagner S.D., Luzzatto L.;
"V kappa gene segments rearranged in chronic lymphocytic leukemia are distributed over a large portion of the V kappa locus and do not show
              ## SCYPDRFSGSGAGTDFTLKISRVEAEDVGVYYCMQVSHFPRTFGGGTRVEIK 132
61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Director MGC Project;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 somatic mutation.";
Eur. J. Immunol. 23:391-397(1993)
                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and mouse cDNA sequences."
                                                                                 CO HUMAN
QÖNBKO HUMAN PRELIMINARY;
QBNEKO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                   IGKV1-5 protein.
                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=8258341;
                                                                                                                                                                                   Name=IGKV1-5;
                                                                      RESULT 11
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 DIVWTQSPLSLPVTPGEPASISCRSSQSLIHSDGYNYLDWYLQKPGQSPQLLIYLGSNRA 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo Sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DVLMTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 SGVPDRFSGSGSGTDFTLKISKVEABDVGIYYCMQGLQTPQTFGQGTKVEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIINE=84191506; PubMed=6325927; Klobeck H.G., Solomon A., Zachau H.G.; "Contribution of human V kappa II germ-line genes to light-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 75.3%; Score 444; DB 2; Length 239; Best Local Similarity 75.0%; Pred. No. 3.4e-39; Matches 84; Conservative 11; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z00009; -; NOT_ANNOTATED_CDS; Genomic_DNA.
PIR; A01889; KZHUGM.
HSSP; Q98M37; 1191.
SMR; P06309; 5: 117.
GO; GO:0005576; C:extracellular region; NAS.
GO; GO:000582; P:amtigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003596; Ig_v.
SMART; SM004066; Ig_v.
PROSTIE; PS50835; IG_LIKE; 1.
Immunoglobulin domain; Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Framework-2.
Complementarity-determining-2.
HSSP, P01834; 1172.

SMR; QNNEKO; 21-237.

InterPro; IPR003105; Ig-like.

InterPro; IPR00306; Ig_MHC.

InterPro; IPR003597; Ig_U.

InterPro; IPR003596; Ig_W.

Pfam; PP0764; IC-set; I.

RMARI; SM00406; IGV; I.

RPOSITE; PS50835; IG_LIKE; 2.

RPOSITE; PS00290; IG_MHC; UNKNOWN_I.

Immunoglobulin domain.

SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552COA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
1g kappa chain V-II region GM607 precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig kappa chain V-II
Framework-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 309:73-76(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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P06309;
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                                                                                                                                      DIVMIQSPLSLPVIPGEPASISCRSSQSLLASNGYNYLDWYLQKPQQSPQLLIYLGSNRA 64
                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                         1 DVLATQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=73166638; PubMed=4700495;
Terry W.D., Page D.L., Kimura S., Isobe T., Osserman B.F.,
Glenner G.G.;
"Structural identity of Bence Jones and amyloid fibril proteins in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 patient with plasma cell dyscrasia and amyloidosis.";
J. Clin. Invest. 52:1276-1281(1973)
-!- MISCELLANEOUS: The major amyloid protein appears to be identical
with the Bence Jones protein isolated from the same patient.
-!- MISCELLANEOUS: This protein was isolated from the urine of a
patient with plasma cell dyscrasia and amyloidosis.
-!- MISCELLANEOUS: The C region of this chain has the INV (1,2)
                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=74148480; PubMed=4596149;
Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
"Amino acid sequence of a kappa Bence Jones protein from a case of
                                                                                                                                                                       61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
                                                                                                                                                                                 ó
                                                                             Length 117;
Complementarity-determining-3. Framework-4. By similarity.
                                                                                                  18; Indels
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Amyloid; Bence-Jones protein; Direct protein sequencing;
Immunoglobulin domain; Immunoglobulin V region.
                                                       12664 MW; 92C57DC719E558B1 CRC64;
                                                                             Score 441; DB 1;
Pred. No. 3.1e-39;
9; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW)
                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-MAY-2005 (Rel. 47, Last annotation update)
19 kappa chain V-II region TEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0005576; C:extracellular region; NAS. GO:0003823; F:antigen binding; NAS. GO; GO:0006955; P:immune response; NAS. InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN SEQUENCE (BENCE-JONES PROTEIN TEW)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochemistry 12:3763-3780(1973).
                                                                             74.7%;
                                                                                                   Conservative
                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                      primary amyloidosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A90370; K2HUTW.
HSSP; Q99M37; 1191.
                                                                 Query Match
Best Local Similarity
85; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; 099M3,,
own: P01617, 1-113.
                                                      117 AA;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi;
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Abbersold R., Herbst H., Grutter T., Chang J.Y., Braun D.G.;
"Murine V kappa 25 and V kappa 27 amino-acid sequences of C57B1/6
origin: monoclonal antibodies 17829.1 and 22825.1 specific for the
group A-streptococcal polysaccharide.";
Hoppe-Seyler's Z. Physiol. Chem. 365:1375-1383 (1984).
-i- FUNCTION: Anti-streptococcal group A carbohydrate antibody.
                                                                                                                                                                                                                                                                                                                                                                                                             61 YGVPDRFSGSGSGTDFTLKISSVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMZALQAPITFGGGTRLEIK 112
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HSSP; Q99M37; 1191.
SMR; P03976; 1-113.
Ensembl; ENSMG500000055315; Mus musculus.
EnterPro; IPR007110; 1g-like.
InterPro; IPR003596; 1g_v.
SMART; SM0466; IGv.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS50836; IG_LIKE; 1.
Interprosipation V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complementarity-determining-1.
Framework-2.
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                    Complementarity-determining-1.
                                                              Complementarity-determining-2.
                                                                                                                                                                                                                                ; Score 438; DB 1; Length 113;
; Pred. No. 6.2e-39;
12; Mismatches 17; Indels
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Complementarity-determining-3.
                                                                                                       Complementarity-determining-3
                                                                                                                                                                                          12316 MW; 0C3C38F81F1843CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-OCT-1986 (Rel. 02, Created)
23-OCT-1986 (Rel. 02, Last sequence update)
19-MAY-2005 (Rel. 47, Last annotation update)
19 kappa chain V-II region 17829.1.
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                                                                                                                                                    By similarity.
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                                            Framework-2.
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MEDLINE=85128968; PubMed=6441768;
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                        1 DVLAMIQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLQWYLQKPGQSPKLLIYKVSNRL
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                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Riesen W.F., Jaton J.-C.;
"Variable region sequence of the light chain from a Waldenstroms IgM
with specificity for phosphorylcholine.";
Biochemistry 15:3829-3833(1976).
-I- MISCELLANEOUS: This chain was isolated from a Waldenstrom's
macroglobulin that binds phosphorylcholine.
                                                                                                                                                                 61 SGVPDRFSSSGSGTDFTLRISRVEAEDVGVYYCAHNLELPYTFGGGTKLEIK 112
                                                                                                                                                   61 YGVPDRFSGSGSGTDFTLKISSVBAEDLGVYYCFQGSHVPWTFGGGTKLEIK 112
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Complementarity-determining-1.
Framework-2.
Complementarity-determining-2.
Framework-3.
                               Length 113;
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                                                           18; Indels
113 AA; 12390 MW; 4E93797046F8DB33 CRC64;
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SMR; P01615; 1-109.
GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0005955; P:immune response; NAS.
InterPro; IPRO0310; Ig-like.
InterPro; IPRO03596; Ig-v.
SMART; SM00406; IGv; 1.
PROSITE; PSS0835; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region.
                             72.2%; Score 426; DB 1; larity 71.4%; Pred. No. 1.2e-37; Conservative 14; Mismatches 18;
                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
MAY-2005 (Rel. 47, Last annotation update)
Ig kappa chain V-II region FR.
                                                                                                                                                                                                                                                        113 AA
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